

144585

Delaval, Jan

From: Liu, Samuel
Sent: Tuesday, February 08, 2005 12:54 PM
To: Delaval, Jan
Subject: 10032361

Hi, Jan,

Please conduct search for amino acid sequences of SEQ ID NOs: 4, 5 and 7 against commercial protein and interference databases, and search for Formula II amino acid sequence of claims 3 and 11 for application 10032361 with at least 50 results, as timely concerned. Note that search for the amino acid sequence of Formula II would be an oligomer search because the claims recite the close-ended language "consisting of ...".

Very best,

Samue Liu
AU 1653, REM 3C84
571-272-0949

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 19:40:51 ; Search time 101.667 Seconds
(without alignments)
72.280 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 95

Sequence: 1 DLDLEMLAXYIPMDDDFOL 19

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	19	4	Aab49912 Human/mur
2	95	100.0	19	6	Aae30166 Peptide #
3	95	100.0	19	6	Aae30167 Peptide #
4	95	100.0	19	6	Aae30144 HIFalpha
5	95	100.0	19	6	Aae30162 Peptide #
6	95	100.0	19	6	Aae30172 Human HIF
7	95	100.0	19	6	Aae30158 HIF-lalphi
8	95	100.0	19	6	Abr82378 Hypoxia-i
9	95	100.0	19	8	Adp56728 Substrate
10	95	100.0	19	8	Adp79479 Hypoxia i
11	95	100.0	20	6	Abp55440 Hypoxia-i
12	95	100.0	20	8	Ado22337 HIF-lalphi
13	95	100.0	29	7	Aao23501 Murine HI
14	95	100.0	29	7	Aao23481 Murine HI
15	95	100.0	29	7	Aao23472 Murine HI
16	95	100.0	29	7	Aao23499 Murine HI
17	95	100.0	30	6	Abr82380 Hypoxia-i
18	95	100.0	34	4	Aab49913 Human/mur
19	95	100.0	34	6	Aae30161 Peptide #
20	95	100.0	34	6	Aae30151 HIFalpha
21	95	100.0	54	3	Aay94637 HIF-lalphi
22	95	100.0	54	7	Aao23490 Murine HI
23	95	100.0	54	7	Aao23530 Murine HI
24	95	100.0	54	7	Aao23528 Murine HI
25	95	100.0	54	7	Aao23519 Murine HI

26	95	100.0	54	7	AAO23529 Murine HI
27	95	100.0	54	7	AAO23493 Murine HI
28	95	100.0	116	3	Aay94632 HIF-lalphi
29	95	100.0	288	3	Aay94633 HIF-lalphi
30	95	100.0	301	3	Aay94634 HIF-lalphi
31	95	100.0	311	3	Aay94631 HIF-lalphi
32	95	100.0	409	8	ADO33389 Chimeric
33	95	100.0	444	8	AAB68415 Amino aci
34	95	100.0	466	8	ADO33390 Chimeric
35	95	100.0	538	8	ADO33387 Chimeric
36	95	100.0	542	5	ABP41474 Human ova
37	95	100.0	595	8	ADO33388 Chimeric
38	95	100.0	613	3	AAY94630 HIF-lalphi
39	95	100.0	613	5	Aau77614 Human hyp
40	95	100.0	632	8	ADO33391 Chimeric
41	95	100.0	652	3	AAY94629 HIF-lalphi
42	95	100.0	669	3	AAY84167 A variant
43	95	100.0	697	3	AAY84166 A variant
44	95	100.0	701	3	AAY84173 A variant
45	95	100.0	710	3	AAY84172 A variant
46	95	100.0	724	3	AAY84171 A variant
47	95	100.0	735	6	ABR82375 Hypoxia-i
48	95	100.0	735	8	ADN75066 Human hyp
49	95	100.0	749	3	AAY84170 A variant
50	95	100.0	756	3	AAY94635 HIF-lalphi
51	95	100.0	789	3	AAY84169 A variant
52	95	100.0	789	6	ADA18535 Human hyp
53	95	100.0	789	6	ADA18533 Human hyp
54	95	100.0	789	6	ADA18534 Human hyp
55	95	100.0	805	2	AAW06558 Hypoxia i
56	95	100.0	810	5	ABBS7270 Mouse lac
57	95	100.0	813	3	AAY94636 HIF-lalphi
58	95	100.0	823	6	ABR41951 Rat hypox
59	95	100.0	825	7	ADD44855 Rat prote
60	95	100.0	826	2	AAW06557 Human hyp
61	95	100.0	826	2	AAW80418 Amino aci
62	95	100.0	826	2	AAY06289 Human tra
63	95	100.0	826	3	AAY69407 A wild ty
64	95	100.0	826	3	AAY94640 Human hyp
65	95	100.0	826	4	AAB76854 Human lun

ALIGNMENTS

RESULT 1	
AAB49912	ID AAB49912 standard; peptide; 19 AA.
XX	
AC	AAB49912;
XX	
DT	06-MAR-2001 (first entry)
XX	
DE	Human/murine HIF-lalphi subunit conserved motif #8.
XX	
KW	Mouse; human; HIF-lalphi; von Hippel-Lindau syndrome protein; VHL;
KW	hypoxia inducible factor-1; cancer; ischaemia.
XX	
OS	Mus sp.
OS	Homo sapiens.
PN	WO200069908-A1.
XX	
PD	23-NOV-2000.
XX	
PF	12-MAY-2000; 2000WO-GB001826.
XX	
PR	12-MAY-1999; 99GB-00011047.
XX	
PA	(ISIS-) ISIS INNOVATION LTD.
XX	
PI	Ratcliffe PJ, Maxwell PH, Pugh CW;
XX	

DR WPI; 2001-025006/03.

XX Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha

PT subunit interaction modulators for treating ischemia by contacting a VHL

PT protein and an HIF subunit protein with a putative modulator.

XX Claim 13; Page 49; 56pp; English.

XX The present invention describes a novel assay for use in identifying

CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible

CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises

CC contacting the VHL protein, the HIF-1alpha subunit and the putative

CC modulator under conditions where the former two would normally complex.

CC Modulators of this type are useful in the treatment of cancer and

CC ischaemic conditions such as coronary, cerebral and vascular

CC insufficiency

XX Sequence 19 AA;

Query Match 100.0%; Score 95; DB 4; Length 19;

Best Local Similarity 94.7%; Pred. NO. 6.4e-08;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19

DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2

AAE30166

ID AAE30166 standard; peptide; 19 AA.

AC AAE30166;

XX 24-FEB-2003 (first entry)

DT Peptide #6 used to block HIF-1alpha/pVHL interaction.

DE Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.

XX Unidentified.

OS WO200274981-A2.

PN 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

PR 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

PA Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

PI WPI; 2003-019808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,

PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,

PT cancer, or inflammatory disorders.

XX Example 1; Page 247; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor

CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and

CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of

CC the invention are used for treating conditions such as ischaemia, wound

CC healing, auto-, allo-, and xeno-transplantation, systemic high blood

CC pressure, cancer, or inflammatory disorders. They are useful in anti-

CC sense regulation of the HIF hydroxylase activity and in particular HIF

CC prolyl hydroxylase activity within a cell. They are also used to identify

CC additional substrates of HIF hydroxylases. Sequences of the invention are

CC used as therapeutic agents and in purification, isolation, or screening

CC methods involving immuno-precipitation techniques and for detecting

CC polypeptides in biological samples. The invention is useful in gene

CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL

CC interaction. This sequence is used in the invention

XX Sequence 19 AA;

Query Match 100.0%; Score 95; DB 6; Length 19;

CC used to design double stranded RNAs for use in RNA interference. They are

CC used as therapeutic agents and in purification, isolation, or screening

CC methods involving immuno-precipitation techniques and for detecting

CC polypeptides in biological samples. The invention is useful in gene

CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL

CC interaction. This sequence is used in the invention

XX Sequence 19 AA;

Query Match 100.0%; Score 95; DB 6; Length 19;

Best Local Similarity 94.7%; Pred. NO. 6.4e-08;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19

DB 1 DLDLEMLAGYIPMDDDFQL 19

RESULT 3

AAE30167

ID AAE30167 standard; peptide; 19 AA.

AC AAE30167;

XX 24-FEB-2003 (first entry)

DT Peptide #7 used to block HIF-1alpha/pVHL interaction.

DE Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.

XX Unidentified.

OS WO200274981-A2.

PN 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

PR 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

PA Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

PI WPI; 2003-019808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,

PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,

PT cancer, or inflammatory disorders.

XX Example 1; Page 247; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor

CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and

CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of

CC the invention are used for treating conditions such as ischaemia, wound

CC healing, auto-, allo-, and xeno-transplantation, systemic high blood

CC pressure, cancer, or inflammatory disorders. They are useful in anti-

CC sense regulation of the HIF hydroxylase activity and in particular HIF

CC prolyl hydroxylase activity within a cell. They are also used to identify

CC additional substrates of HIF hydroxylases. Sequences of the invention are

CC used as therapeutic agents and in purification, isolation, or screening

CC methods involving immuno-precipitation techniques and for detecting

CC polypeptides in biological samples. The invention is useful in gene

CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL

CC interaction. This sequence is used in the invention

XX Sequence 19 AA;

Query Match 100.0%; Score 95; DB 6; Length 19;

```
Best Local Similarity 94.7%; Pred. No. 6.4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 1;

QY 1 DLDLEMLAXIYIPMDDDFQL 19
    |||||:|||||
Db 1 DLDLEMLAXIYIPMDDDFQL 19

RESULT 4
AAE30144
ID AAE30144 standard; peptide; 19 AA.
XX
AC AAE30144;
XX
DT 24-FEB-2003 (first entry)
XX
DE HIFalpha subunit antagonist #1.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW antagonist.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /label= Hyp
FT
XX WO200274981-A2.
XX
XX PD 26-SEP-2002.
XX
XX PF 21-MAR-2002; 2002WO-GB001381.
XX
XX PR 21-MAR-2001; 2001GB-00007123.
XX
XX PR 02-AUG-2001; 2001GB-00018952.
XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX
XX PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX WPI; 2003-018808/01.
XX
XX Novel isolated polypeptide useful for treating ischemia, wound healing,
XX auto-, allo-, and xeno-transplantation, systemic high blood pressure,
XX cancer, or inflammatory disorders.
XX
XX PS Claim 49; Page 196; 256pp; English.
XX
XX The invention relates to polypeptides having hypoxia inducible factor
XX (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
XX 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
XX the invention are used for treating conditions such as ischaemia, wound
XX healing, auto-, allo-, and xeno-transplantation, systemic high blood
XX pressure, cancer, or inflammatory disorders. They are also used to identify
XX additional substrates of HIF hydroxylases. Sequences of the invention are
XX used to design double stranded RNAs for use in RNA interference. They are
XX used as therapeutic agents and in purification, isolation, or screening
XX methods involving immuno-precipitation techniques and for detecting
XX polypeptides in biological samples. The invention is useful in gene
XX therapy. The present sequence is HIFalpha subunit antagonist. This
XX sequence is used in the invention
XX
XX SQ Sequence 19 AA;
    Query Match 100.0%; Score 95; DB 6; Length 19;
    Best Local Similarity 94.7%; Pred. No. 6.4e-08;
    Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXIYIPMDDDFQL 19
    |||||:|||||
Db 1 DLDLEMLAXIYIPMDDDFQL 19

RESULT 6
AAE30172
ID AAE30172 standard; peptide; 19 AA.
XX
AC AAE30172;
XX
DT 24-FEB-2003 (first entry)
XX
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Wed Feb 9 06:11:23 2005

us-10-032-361-5.rag

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XX DE Human HIF1-alpha peptide #2.
XX DE
XX KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW human; HIF1-alpha.
XX KW
XX OS Homo sapiens.
XX PN WO200274981-A2.
XX PD 26-SEP-2002.
XX PF 21-MAR-2002; 2002WO-GB001381.
XX PR 21-MAR-2001; 2001GB-00007123.
XX PR 02-AUG-2001; 2001GB-00018952.
XX XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX XX
XX PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX PD WPI; 2003-018808/01.
XX PF
XX PR Novel isolated polypeptide useful for treating ischemia, wound healing,
XX PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
XX PT cancer, or inflammatory disorders.
XX XX
XX PS Example 1; Page 245; 256pp; English.
XX CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno-precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is HIF-1alpha pVHL minimal binding domain.
XX CC This sequence is used in the invention
XX SQ Sequence 19 AA;
XX
XX Query Match 100.0%; Score 95; DB 6; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 6.4e-08;
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 DLDEMLAXYIPMDDDFQL 19
DB 1 DLDEMLAPYIPMDDDFQL 19
XX
XX RESULT 8
XX ABR82378
XX ID ABR82378 standard; peptide; 19 AA.
XX XX
XX AC ABR82378;
XX XX
XX DT 06-NOV-2003 (first entry)
XX DE Hypoxia-inducible factor 1 (HIF-1) alpha peptide inhibitor.
XX XX
XX KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquilizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 9
XX FT /label= HYP
XX FT /note= "hydroxyproline"
XX XX
XX PN WO2003057820-A2.
XX PD 17-JUL-2003.
XX XX

```

PF 04-OCT-2002; 2002WO-US031699.
 XX
 PR 21-DEC-2001; 2001US-00032361.
 XX
 PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 XX
 PI Mcgrath K;
 XX
 XX WPI; 2003-645988/61.
 XX
 PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
 PT ubiquitination, and activator of vascular endothelial growth factor
 PT transcription useful for treating tissue injuries including wounds,
 PT surgical incisions.
 XX
 XX Claim 2; Page 8; 37pp; English.
 PS
 CC The invention relates to peptide inhibitors of hypoxia-inducible factor,
 CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
 CC transcription of erythropoietin (EPO), vascular endothelial growth factor
 CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
 CC for treating tissue injuries including wounds, surgical incisions,
 CC chronic wounds, heart disease and stroke. The present sequence represents
 CC a specific example of HIF-1 alpha peptide inhibitor, containing the
 CC oxygen-dependent degradation sequence of HIF-1 alpha
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 100.0%; Score 95; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 6.4e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 |||||:|||||
 RESULT 9
 ADP56728
 ID ADP56728 standard; peptide; 19 AA.
 XX
 AC ADP56728;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Substrate peptide used in human HIF prolyl hydroxylase screening assay.
 XX
 KW fat metabolism; HIFalpha; hypoxia inducible factor alpha subunit;
 KW atherosclerosis; diabetes; obesity; HIF prolyl hydroxylase substrate;
 KW human; HIF-PH.
 XX
 OS Homo sapiens.
 XX
 XX WO2004052285-A2.
 PN
 PD 24-JUN-2004.
 XX
 XX 05-DEC-2003; 2003WO-US038690.
 PF
 XX
 PR 06-DEC-2002; 2002US-0431351P.
 PR 06-JUN-2003; 2003US-0476331P.
 PR 06-JUN-2003; 2003US-0476726P.
 PR 04-DEC-2003; 2003US-00729167.
 XX
 XX (FIBR-) FIBROGEN INC.
 PA
 XX Fournay PD, Guenzler-Pukall V, Klaus SJ, Lin AY, Neff TB;
 PI Seeley TW;
 XX
 XX WPI; 2004-468689/44.
 DR
 XX
 XX Regulating fat metabolism or fat metabolic process in subjects, by
 PT stabilizing human foreskin fibroblasts alpha in subject, thus regulating

PT fat metabolism or fat metabolic process in subject.
 XX
 PS Example 9; SEQ ID NO 1; 66pp; English.
 XX
 CC The invention relates to a novel method for regulating fat metabolism or
 CC the fat metabolic process in a subject which comprises stabilising human
 CC foreskin fibroblast HIFalpha (hypoxia inducible factor alpha subunit) in
 CC the subject, or administering a compound that inhibits HIF hydroxylase
 CC activity, thus regulating fat metabolism or the fat metabolic process in
 CC the subject. The method of the invention may be useful for regulating fat
 CC metabolism or a fat metabolic process in a subject. The subject is an
 CC animal, preferably a mammal, more preferably human and the method is
 CC performed in a human cell, tissue or organ. The method may be useful for
 CC treating or preventing atherosclerosis, diabetes and obesity in a
 CC subject. The current sequence is that of the substrate peptide of the
 CC invention which is used during a screening assay of human HIF prolyl
 CC hydroxylase (HIF-PH).
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 95; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 6.4e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 |||||:|||||
 RESULT 10
 ADP79479
 ID ADP79479 standard; peptide; 19 AA.
 XX
 AC ADP79479;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Hypoxia inducible factor prolyl hydroxylase substrate peptide.
 XX
 KW Human; Hypoxia inducible factor prolyl hydroxylase; glucose metabolism;
 KW antidiabetic; anorectic; hypotensive; antiipaeamic; nephrotropic;
 KW neuroprotective; ophthalmological; antiarteriosclerotic; vasotropic;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO2004052284-A2.
 PN
 PD 24-JUN-2004.
 XX
 XX 05-DEC-2003; 2003WO-US038689.
 PF
 XX
 PR 06-DEC-2002; 2002US-0431351P.
 PR 06-JUN-2003; 2003US-0476331P.
 PR 06-JUN-2003; 2003US-0476726P.
 PR 04-DEC-2003; 2003US-00729704.
 XX
 XX (FIBR-) FIBROGEN INC.
 PA
 XX Guenzler-Pukall V, Klaus SJ, Langsetmo Parobok I, Seeley TW;
 PI WPI; 2004-468688/44.
 DR
 XX
 XX Regulating glucose metabolism or glucose metabolic process in subject,
 PT involves stabilizing hypoxia inducible factor alpha in subject, or
 PT administering to subject compound inhibiting hypoxia inducible factor
 PT hydroxylase activity.
 XX
 XX Example 14; SEQ ID NO 5; 74pp; English.
 PS
 CC The present sequence is that of a substrate peptide for hypoxia inducible
 CC factor (HIF) prolyl hydroxylase. It was used in an example from the
 CC invention for the identification of compounds useful for HIF alpha

CC stabilisation. The invention provides methods and compounds for
 CC regulating glucose metabolism by stabilising HIF1 alpha, especially by
 CC administering a compound that inhibits HIF hydroxylase activity. The
 CC method of stabilising HIF1 alpha is used in claimed methods for achieving
 CC glucose homeostasis, decreasing blood glucose levels, decreasing glycated
 CC haemoglobin levels, altering expression of a glucose regulatory factor,
 CC altering expression of a glycolytic factor, treating or preventing
 CC diabetes, treating or preventing a disorder associated with increased
 CC blood glucose levels (especially diabetes, hyperglycaemia, obesity,
 CC hypertension, hyperlipidaemia, nephropathy, neuropathy, retinopathy,
 CC impaired glucose tolerance, atherosclerosis and vascular disease),
 CC treating or preventing a condition associated with diabetes, decreasing
 CC blood triglyceride levels, reducing insulin resistance, and increasing
 CC glycaemic control in a subject.

XX Sequence 19 AA;

Query Match 100.0%; Score 95; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 6.4e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||||
 DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 11
 ABP55440
 ID ABP55440 standard; peptide; 20 AA.

AC ABP55440;

DT 05-FEB-2003 (first entry)

XX Hypoxia-inducible factor (HIF) 1 alpha peptide.

DE Hypoxia; hypoxia-inducible factor; HIF1-alpha; hypoxic-related disorder;
 KW ischaemic-related disorder; hypoxia-inducible factor-related disorder;
 KW prolyl hydroxylation; HIF; hypoxic; ischaemic; vasotropic; cardiatic;
 KW cerebroprotective; cytostatic; thrombolytic; antidiabetic; nephrotropic;
 KW myocardial infarction; heart disease; stroke; cancer; diabetes;
 KW cell-proliferating disorder; deep vein thrombosis; pulmonary embolus;
 KW renal failure; angiogenesis; vascularisation; prolyl hydroxylase.

XX Homo sapiens.

OS Key Location/Qualifiers
 FH Modified-site 9 /label= hydroxyproline

FT WO200274249-A2.

PN 26-SEP-2002.

XX 20-MAR-2002; 2002WO-US008886.

XX 20-MAR-2001; 2001US-0277425P.

PR 20-MAR-2001; 2001US-0277431P.

PR 20-MAR-2001; 2001US-0277440P.

PR 09-NOV-2001; 2001US-0332334P.

PR 09-NOV-2001; 2001US-0332493P.

PR 20-DEC-2001; 2001US-0345200P.

PR 20-DEC-2001; 2001US-0345298P.

PR 20-DEC-2001; 2001US-0345131P.

PR 19-MAR-2002; 2002US-00101812.

XX (DAND) DANA FARBER CANCER INST INC.

XX Kaelin WG, Ivan M;

XX WPI; 2003-058330/05.

PT Treating or preventing a hypoxic- or ischemic-related disorder, e.g.
 PT myocardial infarction, stroke, cancer, thrombosis or renal failure, by
 PT administering a modulator prolyl hydroxylation of hypoxia-inducible
 PT factor (HIF).

XX Disclosure; Page 26; 128pp; English.

XX The present invention describes a method for treating or preventing a
 CC hypoxic-related disorder, ischaemic-related disorder, or hypoxia-
 CC inducible factor (HIF)-related disorder in a subject by administering to
 CC the subject a compound that modulates prolyl hydroxylation of HIF, such
 CC that the hypoxic-, ischaemic-, or HIF-related disorder is treated,
 CC prevented, reversed or stabilised. HIF related sequences can have
 CC vasotropic, cardiatic, cerebroprotective, cytostatic, thrombolytic,
 CC antidiabetic, and nephrotropic activities. The method is useful for
 CC treating hypoxia-related disorder, ischaemic-related disorder or HIF-
 CC related disorder. In particular, the hypoxic- or ischaemic-related
 CC disorder is an acute event (e.g. myocardial infarction, heart disease,
 CC stroke, cancer or cell-proliferating disorder, or diabetes) or a chronic
 CC event (e.g. deep vein thrombosis, pulmonary embolus or renal failure),
 CC especially a chronic event not caused by tissue scarring. The method is
 CC also useful for increasing angiogenesis or vascularisation. The present
 CC sequence represents a human hypoxia-inducible factor 1 alpha (HIF1-alpha)
 CC peptide which is given in the exemplification of the present invention

XX Sequence 20 AA;

Query Match 100.0%; Score 95; DB 6; Length 20;

Best Local Similarity 94.7%; Pred. No. 6.8e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||||
 DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 12

AD022337

ID AD022337 standard; peptide; 20 AA.

XX AC AD022337;

XX 12-AUG-2004 (first entry)

XX HIF1-alpha ligand binding site peptide SEQ ID NO:15.

XX transgenic; transgenic non-human animal; light-generating fusion protein;
 KW ligand binding site; light-generating polypeptide moiety;
 KW hypoxia-inducible factor 1 alpha; HIF-1alpha; hypoxic tissue;
 KW respiratory; cytostatic; vasotropic; virucide; hypoxic condition; cancer;
 KW ischaemia; viral infection; drug screening; drug discovery;
 KW ligand binding site peptide.

XX Homo sapiens.

OS Synthetic.

XX WO2004042361-A2.

XX 21-MAY-2004.

XX 03-NOV-2003; 2003WO-US035154.

XX 04-NOV-2002; 2002US-00287670.

XX (DAND) DANA FARBER CANCER INST INC.

XX Kaelin WG, Livingston DM, Kim T;

XX WPI; 2004-400725/37.

XX New transgenic non-human animal comprising light-generating fusion
 PT protein, useful in diagnosing and treating hypoxic conditions, cancer,
 PT ischemia and viral infections and in drug screening and discovery.

XX Disclosure; SEQ ID NO 15; 111pp; English.

XX The present invention describes a transgenic non-human animal comprising

XX a recombinant nucleic acid molecule stably integrated into the genome of

XX the animal, where the molecule encodes a light-generating fusion protein

XX comprising a ligand binding site and a light-generating polypeptide

XX moiety. Also described: (1) an isolated cell of the animal; (2) producing

XX a transgenic non-human animal; (3) identifying a compound capable of

XX modifying an activity of hypoxia-inducible factor (HIF)-1 alpha; and (4)

XX detecting hypoxic tissue. The compound has respiratory, cytostatic,

XX vasotropic and virucide activities. The transgenic non-human animal,

XX light-generating fusion protein, agents, kits and compositions are useful

XX in diagnosing and treating hypoxic conditions, cancer, ischaemia and

XX viral infections and in drug screening and discovery. The present

XX sequence represents a HIF-1alpha ligand binding site peptide, which is

XX used in the exemplification of the present invention.

SQ Sequence 20 AA;

Query Match 100.0%; Score 95; DB 8; Length 20;

Best Local Similarity 94.7%; Pred. No. 6.8e-08;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19

Db 1 DLDLEMLAPYIPMDDDFQL 19

|||||:|||||

RESULT 13

AAO233501

ID AAO23501 standard; peptide; 29 AA.

XX AAO23501;

XX 12-FEB-2004 (first entry)

XX Murine HIF-1alpha protein N-TAD region mutant fragment P563A.

XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;

XX ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;

XX antarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;

XX N-TAD; mutant.

XX Mus sp.

XX WO2003074560-A2.

XX 12-SEP-2003.

XX 05-MAR-2003; 2003WO-SE000372.

XX 05-MAR-2002; 2002US-0361333P.

XX 27-NOV-2002; 2002US-0429307P.

XX (ANGI-) ANGIOGENETICS SWEDEN AB.

XX Pereira T, Poellinger L, Hellstroem M;

XX WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing

XX angiogenesis, or treating a condition associated with HIF-1alpha

XX underexpression in a cell, a group of cells, or an organism, e.g.

XX ischemia or inflammation.

XX Example 6; Fig 19; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein

XX that has (a) an altered transactivation capacity and improved stability

XX at normoxia. The HIF-1alpha protein, polynucleotide, vector, and

XX pharmaceutical composition are useful for increasing angiogenesis,

XX interfering with a normal response to reoxygenation following hypoxia, or

XX response in a cell, group of cells, or organism, inducing vascular

CC treating a condition associated with HIF-1alpha underexpression in a

CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic

CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,

CC stroke. The proteins and pharmaceutical compositions are also useful for

CC mimicking the hypoxic response or artificially inducing a hypoxic

CC response in a cell, group of cells, or organism, inducing vascular

CC formation or vascular development in a cell or a group of cells,

CC increasing angiogenic activity in a cell, or influencing erythropoietin

CC production, metabolism, or an inflammatory response in a cell, a group of

CC cells, or an organism. Sequences AAO23500-509 represent mutant fragments

CC within the N-TAD region of a murine HIF-1 alpha protein

XX Sequence 29 AA;

SQ

Query Match 100.0%; Score 95; DB 7; Length 29;

Best Local Similarity 94.7%; Pred. No. 1e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19

Db 10 DLDLEMLAAYIPMDDDFOL 28

|||||:|||||

RESULT 14

AAO23481

ID AAO23481 standard; peptide; 29 AA.

XX AAO23481;

XX 12-FEB-2004 (first entry)

XX Murine HIF-1alpha protein mutant fragment.

XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;

XX ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;

XX antarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;

XX mutant.

XX Mus sp.

XX WO2003074560-A2.

XX 12-SEP-2003.

XX 05-MAR-2003; 2003WO-SE000372.

XX 05-MAR-2002; 2002US-0361333P.

XX 27-NOV-2002; 2002US-0429307P.

XX (ANGI-) ANGIOGENETICS SWEDEN AB.

XX Pereira T, Poellinger L, Hellstroem M;

XX WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing

XX angiogenesis, or treating a condition associated with HIF-1alpha

XX underexpression in a cell, a group of cells, or an organism, e.g.

XX ischemia or inflammation.

XX Claim 39; Page 93; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein

XX that has (a) an altered transactivation capacity and improved stability

XX at normoxia. The HIF-1alpha protein, polynucleotide, vector, and

XX pharmaceutical composition are useful for increasing angiogenesis,

XX interfering with a normal response to reoxygenation following hypoxia, or

XX treating a condition associated with HIF-1alpha underexpression in a

XX cell, a group of cells, or an organism, e.g. ischaemia, diabetic

XX retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,

XX stroke. The proteins and pharmaceutical compositions are also useful for

XX mimicking the hypoxic response or artificially inducing a hypoxic

XX response in a cell, group of cells, or organism, inducing vascular

CC formation or vascular development in a cell or a group of cells.
CC increasing angiogenic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a specific example
CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-
CC related conditions

XX Sequence 29 AA;

Query Match 100.0%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||:|||||
DB 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 15

AAO23472
ID AAO23472 standard; peptide; 29 AA.

XX AAO23472;

DT 12-FEB-2004 (first entry)

DE Murine HIF-1alpha protein mutant fragment.

KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW mutant.

OS Mus sp.

PN WO2003074560-A2.

PD 12-SEP-2003.

PF 05-MAR-2003; 2003WO-SE000372.

PR 05-MAR-2002; 2002US-0361333P.

PR 27-NOV-2002; 2002US-0429307P.

PA (ANGI-) ANGIOGENETICS SWEDEN AB.

PI Persira T, Poellinger L, Hellstroem M;

XX WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.

PS Claim 39; Page 89; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells.
CC increasing angiogenic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a specific example
CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-

CC related conditions

XX Sequence 29 AA;

Query Match 100.0%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||:|||||
DB 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 16

AAO23499
ID AAO23499 standard; peptide; 29 AA.

XX AAO23499;

DT 12-FEB-2004 (first entry)

DE Murine HIF-1alpha protein N-TAD region fragment (residues 546-573).

KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD.

OS Mus sp.

PN WO2003074560-A2.

PD 12-SEP-2003.

PF 05-MAR-2003; 2003WO-SE000372.

PR 05-MAR-2002; 2002US-0361333P.

PR 27-NOV-2002; 2002US-0429307P.

PA (ANGI-) ANGIOGENETICS SWEDEN AB.

PI Persira T, Poellinger L, Hellstroem M;

XX WPI; 2003-712876/67.

XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.

PS Example 6; Fig 19; 96pp; English.

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells.
CC increasing angiogenic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a N-TAD region of
CC a murine HIF-1 alpha protein

XX Sequence 29 AA;

Query Match 100.0%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 1e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 Dd 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 17
 ABR82380
 ID ABR82380 standard; peptide; 30 AA.

AC ABR82380;

XX 06-NOV-2003 (first entry)

DE Hypoxia-inducible factor 1 (HIF-1) alpha inhibitor ODD peptide.

KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
 KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
 KW tranquilizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
 XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 20
 FT /label= Hyp
 FT /note= "hydroxyproline"

PN WO2003057820-A2.

XX 17-JUL-2003.

XX 04-OCT-2002; 2002WO-US031699.

XX 21-DEC-2001; 2001US-00032361.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Mcgrath K;

XX WPI; 2003-645988/61.

XX Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
 PT ubiquitination, and activator of vascular endothelial growth factor
 PT transcription useful for treating tissue injuries including wounds,
 PT surgical incisions.

XX Claim 2; Page 9; 37pp; English.

XX The invention relates to peptide inhibitors of hypoxia-inducible factor
 CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
 CC transcription of erythropoietin (EPO), vascular endothelial growth factor
 CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
 CC for treating tissue injuries including wounds, surgical incisions,
 CC chronic wounds, heart disease and stroke. The present sequence represents
 CC an ODD peptide, a specific example of HIF-1 alpha peptide inhibitor,
 CC containing the oxygen-dependent degradation sequence of HIF-1 alpha

XX Sequence 30 AA;

Query Match 100.0%; Score 95; DB 6; Length 30;
 Best Local Similarity 94.7%; Pred. No. 1.1e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 Dd 12 DLDLEMLAPYIPMDDDFQL 30

RESULT 18
 AAB49913
 ID AAB49913 standard; peptide; 34 AA.

XX

AC AAB49913;
 XX 06-MAR-2001 (first entry)
 XX Human/murine HIF-1alpha subunit conserved motif #9.
 DE Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
 KW hypoxia inducible factor-1; cancer; ischaemia.
 XX Mus sp.
 OS Homo sapiens.
 XX WO200069908-A1.
 XX 23-NOV-2000.
 XX 12-MAY-2000; 2000WO-GB001826.
 XX 12-MAY-1999; 99GB-00011047.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Ratcliffe PJ, Maxwell PH, Pugh CW;
 PI WPI; 2001-025006/03.
 DR Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
 PT subunit interaction modulators for treating ischemia by contacting a VHL
 PT protein and an HIF subunit protein with a putative modulator.
 XX Claim 14; Page 50; 56pp; English.
 XX The present invention describes a novel assay for use in identifying
 CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
 CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
 CC contacting the VHL protein, the HIF-1alpha subunit and the putative
 CC modulator under conditions where the former two would normally complex.
 CC Modulators of this type are useful in the treatment of cancer and
 CC ischaemic conditions such as coronary, cerebral and vascular
 CC insufficiency
 XX Sequence 34 AA;
 XX Query Match 100.0%; Score 95; DB 4; Length 34;
 XX Best Local Similarity 94.7%; Pred. No. 1.2e-07;
 XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DLDLEMLAXYIPMDDDFQL 19
 Dd 8 DLDLEMLAPYIPMDDDFQL 26
 XX RESULT 19
 XX AAE30161
 ID AAE30161 standard; peptide; 34 AA.
 XX AAE30161;
 XX AC AAE30161;
 XX 24-FEB-2003 (first entry)
 XX Peptide #1 used to block HIF-1alpha/pVHL interaction.
 DE Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
 KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
 XX Unidentified.
 OS WO200274981-A2.
 XX 26-SEP-2002.
 XX 21-MAR-2002; 2002WO-GB001381.
 XX

PR	21-MAR-2001; 2001GB-00007123.
PR	02-AUG-2001; 2001GB-00018952.
XX	(ISIS-) ISIS INNOVATION LTD.
XX	Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
PI	WPI; 2003-018808/01.
DR	
XX	
PT	Novel isolated polypeptide useful for treating ischemia, wound healing,
PT	auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT	cancer, or inflammatory disorders.
XX	
XX	Example 1; Page 246; 256pp; English.
CC	The invention relates to polypeptides having hypoxia inducible factor
CC	(HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC	3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC	the invention are used for treating conditions such as ischemia, wound
CC	healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC	pressure, cancer, or inflammatory disorders. They are useful in anti-
CC	sense regulation of the HIF hydroxylase activity and in particular HIF
CC	prolyl hydroxylase activity within a cell. They are also used to identify
CC	additional substrates of HIF hydroxylases. Sequences of the invention are
CC	used to design double stranded RNAs for use in RNA interference. They are
CC	used as therapeutic agents and in purification, isolation, or screening
CC	methods involving immuno-precipitation techniques and for detecting
CC	polypeptides in biological samples. The invention is useful in gene
CC	therapy. The present sequence is a peptide used to block HIF-1alpha/pvHL
CC	interaction. This sequence is used in the invention
XX	
SQ	Sequence 34 AA;
Query Match	100.0%; Score 95; DB 6; Length 34;
Best Local Similarity	94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 DLDLEMLAXIIPMDDDFQL 19 : 8 DLDLEMLAPIPMDDDFQL 26
DB	
RESULT 20	
AAE30151	
ID	AAE30151 standard; peptide; 34 AA.
XX	
AC	AAE30151;
DT	24-FEB-2003 (first entry)
XX	
DE	HIFalpha subunit antagonist #8.
XX	
KW	Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW	wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW	antagonist.
XX	
OS	Unidentified.
XX	
PV	WO200274981-A2.
XX	
PD	26-SEP-2002.
XX	
XX	21-MAR-2002; 2002WO-GB001381.
XX	
PR	21-MAR-2001; 2001GB-00007123.
PR	02-AUG-2001; 2001GB-00018952.
XX	
XX	(ISIS-) ISIS INNOVATION LTD.
PA	
PI	Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX	
DR	WPI; 2003-018808/01.
XX	

CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aqueora victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of
 CC angiogenesis, erythropoiesis and glycolysis
 XX
 SQ Sequence 54 AA;

Query Match 100.0%; Score 95; DB 3; Length 54;
 Best Local Similarity 94.7%; Pred. No. 2.1e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 26 DLDLEMLAPYIPMDDDFQL 44

RESULT 22
 AAO23490
 ID AAO23490 standard; peptide; 54 AA.
 AC AAO23490;
 DT 12-FEB-2004 (first entry)
 DE Murine HIF-1alpha protein N-TAD region fragment (residues 531-584).
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD.

OS Mus sp.
 XX WO2003074560-A2.
 FN 05-MAR-2003; 2003WO-SE000372.
 PD 12-SEP-2003.
 XX 05-MAR-2003; 2003WO-SE000372.
 PF 05-MAR-2002; 2002US-0361333P.
 PR 27-NOV-2002; 2002US-0429307P.
 XX (ANGI-) ANGIOGENETICS SWEDEN AB.
 PA Pereira T, Poellinger L, Hellstroem M;
 XX WPI; 2003-712876/67.
 DR
 XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX Example 4; Fig 4; 96pp; English.

PS The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,

CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;

Query Match 100.0%; Score 95; DB 7; Length 54;
 Best Local Similarity 94.7%; Pred. No. 2.1e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 23
 AAO23530
 ID AAO23530 standard; peptide; 54 AA.
 XX AAO23530;
 AC AAO23530;
 DT 12-FEB-2004 (first entry)
 DE Murine HIF-1alpha protein N-TAD region mutant fragment Q572A.

KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.

OS Mus sp.
 XX WO2003074560-A2.
 FN 12-SEP-2003.
 PD 05-MAR-2003; 2003WO-SE000372.
 PF 05-MAR-2002; 2002US-0361333P.
 PR 27-NOV-2002; 2002US-0429307P.
 XX (ANGI-) ANGIOGENETICS SWEDEN AB.
 PA Pereira T, Poellinger L, Hellstroem M;
 XX WPI; 2003-712876/67.

PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX Example 11; Fig 27; 96pp; English.

PS The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of

CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein

SQ Sequence 54 AA;

Query Match 100.0%; Score 95; DB 7; Length 54;

Best Local Similarity 94.7%; Pred. No. 2.1e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 24

AAO23528

ID AAO23528 standard; peptide; 54 AA.

XX AC AAO23528;

DT 12-FEB-2004 (first entry)

DE Murine HIF-1alpha protein N-TAD region mutant fragment L573A.

XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.

XX OS Mus sp.

XX PN WO2003074560-A2.

XX PD 12-SEP-2003.

XX PF 05-MAR-2003; 2003WO-SE000372.

XX PR 05-MAR-2002; 2002US-0361333P.

XX PR 27-NOV-2002; 2002US-0429307P.

XX PA (ANGI-) ANGIOGENETICS SWEDEN AB.

XX PI Pereira T, Poellinger L, Hellstroem M;

XX DR WPI; 2003-712876/67.

XX PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX PS Example 11; Fig 27; 96pp; English.

XX CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein

SQ Sequence 54 AA;

Query Match 100.0%; Score 95; DB 7; Length 54;

Best Local Similarity 94.7%; Pred. No. 2.1e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 25

AAO23519

ID AAO23519 standard; peptide; 54 AA.

XX AC AAO23519;

DT 12-FEB-2004 (first entry)

DE Murine HIF-1alpha protein N-TAD region mutant fragment P563A.

XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.

XX OS Mus sp.

XX PN WO2003074560-A2.

XX PD 12-SEP-2003.

XX PF 05-MAR-2003; 2003WO-SE000372.

XX PR 05-MAR-2002; 2002US-0361333P.

XX PR 27-NOV-2002; 2002US-0429307P.

XX PA (ANGI-) ANGIOGENETICS SWEDEN AB.

XX PI Pereira T, Poellinger L, Hellstroem M;

XX DR WPI; 2003-712876/67.

XX PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.

XX PS Example 11; Fig 27; 96pp; English.

XX CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein

SQ Sequence 54 AA;

Query Match 100.0%; Score 95; DB 7; Length 54;

Best Local Similarity 94.7%; Pred. No. 2.1e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 25 DLDLEMLAPYIPMDDDFQL 43

```

RESULT 26
AAO23529
ID AAO23529 standard; peptide; 54 AA.
XX
AC AAO23529;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment QR-A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
XX
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 11; Fig 27; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 100.0%; Score 95; DB 7; Length 54;
Best Local Similarity 94.7%; Pred. No. 2.1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
DB 25 DLDLEMLAAYIPMDDDFQL 43

RESULT 27
AAO23493
ID AAO23493 standard; peptide; 54 AA.
XX
AC AAO23493;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/526-641.
XX

```

KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 OS Homo sapiens.
 XX WO200029437-A1.
 PN 25-MAY-2000.
 XX 11-NOV-1999; 99WO-SE002053.
 XX 13-NOV-1998; 98SE-00003891.
 XX (PHAA) PHARMACIA & UPJOHN AB.
 PA Berkenstam A, Poellinger L;
 PI WPI; 2000-399715/34.
 DR Human hypoxia-inducible factor alpha variants for identifying compounds
 XX that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 PT Claim 13; Page 76-77; 87pp; English.
 XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584.
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of HIF-
 CC angiogenesis, erythropoiesis an glycolysis
 XX Sequence 116 AA;
 SQ Query Match 100.0%; Score 95; DB 3; Length 116;
 Best Local Similarity 94.7%; Pred. No. 5.1e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDEMLAXYIPMDDDFQL 19
 DB 31 DLDEMLAPYIPMDDDFQL 49
 RESULT 29
 AAY94633
 ID AAY94633 standard; protein; 288 AA.
 XX AAY94633;
 AC 15-AUG-2000 (first entry)
 DT HIF-1alpha variant protein sequence HIF-1alpha/526-813.
 XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX Homo sapiens.
 OS WO200029437-A1.
 PN 25-MAY-2000.
 XX 11-NOV-1999; 99WO-SE002053.
 XX 13-NOV-1998; 98SE-00003891.
 XX (PHAA) PHARMACIA & UPJOHN AB.

PD 25-MAY-2000.
 XX 11-NOV-1999; 99WO-SE002053.
 XX 13-NOV-1998; 98SE-00003891.
 XX (PHAA) PHARMACIA & UPJOHN AB.
 PA Berkenstam A, Poellinger L;
 PI WPI; 2000-399715/34.
 DR Human hypoxia-inducible factor alpha variants for identifying compounds
 XX that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 PT Claim 13; Page 77-78; 87pp; English.
 XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584.
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of HIF-
 CC angiogenesis, erythropoiesis an glycolysis
 XX Sequence 288 AA;
 SQ Query Match 100.0%; Score 95; DB 3; Length 288;
 Best Local Similarity 94.7%; Pred. No. 1.4e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDEMLAXYIPMDDDFQL 19
 DB 31 DLDEMLAPYIPMDDDFQL 49
 RESULT 30
 AAY94634
 ID AAY94634 standard; protein; 301 AA.
 XX AAY94634;
 AC 15-AUG-2000 (first entry)
 DT HIF-1alpha variant protein sequence HIF-1alpha/526-826.
 XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX Homo sapiens.
 OS WO200029437-A1.
 PN 25-MAY-2000.
 XX 11-NOV-1999; 99WO-SE002053.
 XX 13-NOV-1998; 98SE-00003891.
 XX (PHAA) PHARMACIA & UPJOHN AB.

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XX Berkenstam A, Poellinger L;
PI WPI; 2000-399715/34.
XX Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX Claim 13; Page 78-79; 87pp; English.
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of HIF-
CC angiogenesis, erythropoiesis an glycolysis
XX Sequence 301 AA;
SQ
    Query Match          100.0%; Score 95; DB 3; Length 301;
    Best Local Similarity 94.7%; Pred. No. 1.5e-06;
    Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
Db 31 DLDLEMLAPYIPMDDDFQL 49
    |||||:|||||
    226 DLDLEMLAPYIPMDDDFQL 244

RESULT 31
RAY94631
ID AAY94631 standard; protein; 311 AA.
XX
AC AAY94631;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/331-641.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
PI WPI; 2000-399715/34.
XX
DR Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
```

```
PT angiogenesis, erythropoiesis.
XX Claim 13; Page 74-75; 87pp; English.
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of HIF-
CC angiogenesis, erythropoiesis an glycolysis
XX Sequence 311 AA;
SQ
    Query Match          100.0%; Score 95; DB 3; Length 311;
    Best Local Similarity 94.7%; Pred. No. 1.6e-06;
    Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
Db 226 DLDLEMLAPYIPMDDDFQL 244
    |||||:|||||

RESULT 32
ADO39389
ID ADO39389 standard; protein; 409 AA.
XX
AC ADO39389;
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #3.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39384.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
```

PS Disclosure; Fig 6H; 28pp; English.

XX The invention describes an isolated polynucleotide (I) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions; an isolated polynucleotide which codes for the chimeric
 CC transactivator (1); a vector comprising the chimeric transactivator
 CC polynucleotide (2); a composition comprising polynucleotide (2) and a
 CC polynucleotide which contains a sequence that codes for a target gene and
 CC a promoter which is regulated by the chimeric transactivator coded; a
 CC method of expressing a target gene in a subject, comprising administering
 CC the composition of (4); a method of increasing the number of red blood
 CC cells in a subject, comprising administering the composition of (4) to
 CC the subject; and a method of increasing the number of blood vessels in
 CC subject, comprising administering the composition of (4) to the subject.
 CC The methods and compositions of the present invention are useful for
 CC treating anaemia associated with AIDS or cancer, anaemia from
 CC inflammatory origin and haemoglobinopathies. This is the amino acid
 CC sequence of a fragment of a chimeric transactivator comprising regions of
 CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
 CC transcription factor gene and VP16.

XX SQ Sequence 409 AA;

Query Match 100.0%; Score 95; DB 8; Length 409;
 Best Local Similarity 94.7%; Pred. No. 2.2e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 DB 235 DLDLEMLAPYIPMDDDFQL 253

RESULT-337
 AAB68415
 ID AAB68415 standard; protein; 444 AA.
 XX AAB68415;
 AC AAB68415;
 XX 23-JUL-2001 (first entry)
 DT Amino acid sequence of tTAK-hH104.
 DE Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
 XX anemia; cancer; ischemia; erythropoietin; immunotherapy;
 KW autoimmune disease; hH104; tTAK.
 KW Synthetic.
 XX WO200136616-A2.
 PN 25-MAY-2001.
 XX 17-NOV-2000; 2000WO-FR003207.
 XX 18-NOV-1999; 99FR-00014513.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX (AVET) AVENTIS PHARMA SA.
 XX Beuzard Y, Payen E, Scherman D, Bettan M;
 PI WPI; 2001-343818/36.
 DR N-PSDB; AAF85323.
 XX New nucleic acid construct for controlling expression of target gene,
 PT useful e.g. for treating cancer, is modulated by exogenous
 PT pharmaceutical and oxygen partial pressure.
 XX Disclosure; Page 57-58; 60pp; French.

XX The specification describes a nucleic acid construct bearing a system for
 CC regulating the expression of a gene. The nucleic acid construct comprises
 CC at least one sequence encoding a protein that regulates expression of at
 CC least one gene of interest. The activity of this protein is modulated by
 CC presence/absence of a pharmacological agent and the amount of protein
 CC produced depends on the oxygen partial pressure. The constructs are used
 CC to treat conditions associated with cellular hypoxia, especially anemia,
 CC cancer and ischemia, specifically where the gene of interest encodes
 CC erythropoietin (but many other suitable genes are listed, e.g. those
 CC encoding single-chain antibodies for immunotherapy of infections or
 CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
 CC etc.). The present sequence is encoded by the open reading frame of tTAK-
 CC hH104. The sequence contains a human hH104 fragment, inserted into the
 CC BSIWI site of tTAK. The sequence is used to produce constructs of the
 CC invention

XX SQ Sequence 444 AA;

Query Match 100.0%; Score 95; DB 4; Length 444;
 Best Local Similarity 94.7%; Pred. No. 2.4e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 DB 242 DLDLEMLAPYIPMDDDFQL 260

RESULT 34
 ADO39390
 ID ADO39390 standard; protein; 466 AA.
 XX ADO39390;
 AC ADO39390;
 XX 15-JUL-2004 (first entry)
 DT Chimeric transactivator THV fragment #4.
 DE haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.
 XX Homo sapiens.
 OS US2004018606-A1.
 PN 29-JAN-2004.
 XX 30-APR-2003; 2003US-00425833.
 XX 30-APR-2002; 2002US-0376269P.
 XX (BOHL/) BOHL D.
 XX (HEAR/) HEARD M.
 XX Bohl D, Heard M;
 XX WPI; 2004-122040/12.
 DR N-PSDB; ADO39385.
 XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
 PT of a transcription factor susceptible to degradation under normoxia
 PT conditions, useful for treating anemia associated with AIDS, cancer and
 PT inflammation.
 XX Disclosure; Fig 6I; 28pp; English.

XX The invention describes an isolated polynucleotide (I) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the

transcription factor susceptibility to degradation under normoxia conditions; an isolated polynucleotide which codes for the chimeric transactivator (1); a vector comprising the chimeric transactivator polynucleotide (2); a composition comprising polynucleotide (2) and a polynucleotide which contains a sequence that codes for a target gene and a promoter which is regulated by the chimeric transactivator coded; a method of expressing a target gene in a subject, comprising administering the composition of (4); a method of increasing the number of red blood cells in a subject, comprising administering the composition of (4) to the subject; and a method of increasing the number of blood vessels in the subject, comprising administering the composition of (4) to the subject. The methods and compositions of the present invention are useful for treating anaemia associated with AIDS or cancer, anaemia from inflammatory origin and haemoglobinopathies. This is the amino acid sequence of a fragment of a chimeric transactivator comprising regions of the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1) transcription factor gene and VP16.

XX Sequence 466 AA;

Query Match 100.0%; Score 95; DB 8; Length 466;
 Best Local Similarity 94.7%; Pred. No. 2.5e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 35
 ADO39387
 ID ADO39387 standard; protein; 538 AA.
 AC ADO39387;
 XX
 XX
 DT 15-JUL-2004 (first entry)
 DE
 XX Chimeric transactivator THV fragment #1.
 KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.
 XX
 OS Homo sapiens.
 XX
 PN US2004018606-A1.
 PD 29-JAN-2004.
 XX
 XX 30-APR-2003; 2003US-00425833.
 XX
 PR 30-APR-2002; 2002US-0376269P.
 XX
 XX (BOHL/) BOHL D.
 PA (HEAR/) HEAR M.
 XX
 XX Bohl D, Heard M;
 XX
 XX WPI; 2004-122040/12.
 DR N-PSDB; ADO39382.
 XX
 XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain of a transcription factor susceptible to degradation under normoxia conditions, useful for treating anemia associated with AIDS, cancer and inflammation.
 XX
 PS Disclosure; Fig 6F; 28pp; English.
 XX
 XX The invention describes an isolated polynucleotide (1) which codes for a domain of a transcription factor, wherein the domain confers to the transcription factor susceptibility to degradation under normoxia conditions. Also described are: a chimeric transactivator comprising a

domain of a transcription factor, wherein the domain confers to the transcription factor susceptibility to degradation under normoxia conditions; an isolated polynucleotide which codes for the chimeric transactivator (1); a vector comprising the chimeric transactivator polynucleotide (2); a composition comprising polynucleotide (2) and a polynucleotide which contains a sequence that codes for a target gene and a promoter which is regulated by the chimeric transactivator coded; a method of expressing a target gene in a subject, comprising administering the composition of (4); a method of increasing the number of red blood cells in a subject, comprising administering the composition of (4) to the subject; and a method of increasing the number of blood vessels in the subject, comprising administering the composition of (4) to the subject. The methods and compositions of the present invention are useful for treating anaemia associated with AIDS or cancer, anaemia from inflammatory origin and haemoglobinopathies. This is the amino acid sequence of a fragment of a chimeric transactivator comprising regions of the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1) transcription factor gene and VP16.

XX Sequence 538 AA;

Query Match 100.0%; Score 95; DB 8; Length 538;
 Best Local Similarity 94.7%; Pred. No. 3e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 36
 ABP41474
 ID ABP41474 standard; protein; 542 AA.
 XX
 AC ABP41474;
 XX
 DT 22-AUG-2002 (first entry)
 DE
 XX Human ovarian antigen HNOBJ10, SEQ ID NO:2606.
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 14q21-24.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 XX 03-JAN-2002.
 XX
 XX 07-JUN-2001; 2001WO-US018569.
 XX
 XX 07-JUN-2000; 2000US-0209467P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Birse CE, Rosen CA;
 XX WPI; 2002-147878/19.
 DR N-PSDB; ABQ54551.
 XX
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

PS Claim 11; SEQ ID NO 2606; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 542 AA;

Query Match 100.0%; Score 95; DB 5; Length 542;
Best Local Similarity 94.7%; Pred. NO. 3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||

Db 272 DLDLEMLAPYIPMDDDFQL 290
|||||:|||||

RESULT 37

AD039388

ID AD039388 standard; protein; 595 AA.

XX AC AD039388;

XX DT 15-JUL-2004 (first entry)

XX DE Chimeric transactivator THV fragment #2.

XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.

XX OS Homo sapiens.

XX FN US2004018606-A1.

XX PD 29-JAN-2004.

XX PF 30-APR-2003; 2003US-00425833.

XX PR 30-APR-2002; 2002US-0376269P.

XX (BOHL/) BOHL D.

XX PA (HEAR/) HEAR M.

XX FI Bohl D, Heard M;

XX DR WPI; 2000-399715/34.

XX

DR WPI; 2004-122040/12.

DR N-ESDB; ADO39383.

XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.

XX Disclosure; Fig 6G; 28pp; English.

PS The invention describes an isolated polynucleotide (1) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.

SQ Sequence 595 AA;

Query Match 100.0%; Score 95; DB 8; Length 595;
Best Local Similarity 94.7%; Pred. No. 3.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||

Db 364 DLDLEMLAPYIPMDDDFQL 382
|||||:|||||

RESULT 38

AA94630

ID AA94630 standard; protein; 613 AA.

XX AC AA94630;

XX DT 15-AUG-2000 (first entry)

XX DE HIF-1alpha variant protein sequence HIF-1alpha/delta178-390.

XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX OS Homo sapiens.

XX FN WO2000029437-A1.

XX PD 25-MAY-2000.

XX PF 11-NOV-1999; 99WO-SE002053.

XX PR 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX PI Berkenstam A, Poellinger L;

XX DR WPI; 2000-399715/34.

XX

PT Human hypoxia-inducible factor alpha variants for identifying compounds
 PT that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 XX
 XX
 PS Claim 13; Page 72-74; 87pp; English.
 CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes. The compounds are useful for the regulation of HIF-
 CC angiogenesis, erythropoiesis and glycolysis
 XX
 SQ Sequence 613 AA;
 Query Match 100.0%; Score 95; DB 3; Length 613;
 Best Local Similarity 94.7%; Pred. No. 3.4e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 343 DLDLEMLAPYIPMDDDFQL 361
 RESULT 39
 AAU77614
 ID AAU77614 standard; protein; 613 AA.
 XX
 AC AAU77614;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human hypoxia-inducible factor-1 alpha, HIF-1, mutant delta 178-390.
 XX
 KW Human; HIF-1; hypoxia-inducible factor-1; rheumatoid arthritis;
 KW transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction;
 KW circulatory disorder; cancer; hypertension; demyelinating disorder;
 KW angiogenesis; sarcoidosis; hepatitis-caused inflammation;
 KW chronic ulceration; neovascularisation; arterial hypervascularisation;
 KW bullous skin disease; vasculitis; dermatomyositis; mutant;
 KW mutin; Y565G.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 177..178
 FT /note= "Residues 178-390 of the wild-type HIF-1 have been
 FT deleted"
 FT
 XX
 PN WO200212326-A2.
 XX
 PD 14-FEB-2002.
 XX
 XX
 PF 07-AUG-2001; 2001WO-IB001775.
 XX
 PR 07-AUG-2000; 2000US-0223480P.
 XX
 XX (ASPE-) ASPERA PHARM AB.
 PA
 XX

PI Poellinger L, Pereira T, Ruas J;
 XX
 DR WPI; 2002-257466/30.
 XX
 PT New polypeptides comprising hypoxia-inducible factor-1 with alterations
 PT of the transactivation domain, useful treating ischemic conditions, e.g.
 PT brain infarction, heart infarction or circulatory disorder.
 XX
 PS Example 5; Page; 80pp; English.
 CC The invention relates to a polypeptide comprising hypoxia-inducible
 CC factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or
 CC C-TAD). Also included are nucleic acids encoding the altered proteins, a
 CC vector comprising the nucleic acid, a host cell transformed with the
 CC vector, methods for producing the protein or its functional fragment or
 CC an isolated degradation box, a method of screening for an agent that
 CC modulates N-TAD function and antagonists, agonists, modulators and HIF-1
 CC peptide fragments useful for modulating HIF-1 function or the function of
 CC proteins that interact with it. The isolated polypeptides and their
 CC fragments with altered residues are useful in methods for treating
 CC diseases. The disease is an ischaemic condition, e.g. brain infarction,
 CC heart infarction or circulatory disorder. The disease may also be cancer,
 CC hypertension, demyelinating disorders, diffuse proliferative
 CC glomerulonephritis, toxoplasmosis caused retinohorioiditis, HIV (human
 CC immunodeficiency virus) caused Tat angiogenesis, HIV-caused Kaposi's
 CC sarcoma, hepatitis-caused inflammation, hepatitis-caused angiodysplasia,
 CC chronic ulceration, proliferative retinopathy, retina haemangioblastomas,
 CC neovascularisation, arterial hypervascularisation, sarcoidosis, bullous
 CC skin disease, vasculitis with angiogenesis, dermatomyositis with
 CC angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis,
 CC juvenile osteoarthritis, polyarthritis, aneurysm or atheroma. The present
 CC sequence represents HIF-1 mutant delta 178-390. Note: The present
 CC sequence is not shown in the specification but was created by the indexer
 CC using the information in example 5 and the HIF sequence appearing as
 XX AAU77602
 XX
 SQ Sequence 613 AA;
 Query Match 100.0%; Score 95; DB 5; Length 613;
 Best Local Similarity 94.7%; Pred. No. 3.4e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 Db 343 DLDLEMLAPYIPMDDDFQL 361
 RESULT 40
 ADO39391
 ID ADO39391 standard; protein; 632 AA.
 XX
 AC ADO39391;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Chimeric transactivator THV fragment #5.
 DE
 XX
 KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.
 XX
 OS Homo sapiens.
 OS
 XX US2004018606-A1.
 PN
 XX 29-JAN-2004.
 PD
 XX 30-APR-2003; 2003US-00425833.
 PF
 XX 30-APR-2002; 2002US-0376269P.
 PR
 XX (BOHL/) BOHL D.
 PA

PA (HEAR/) HEARD M.
 XX
 PI Bohl D, Heard M;
 XX
 DR WPI; 2004-122040/12.
 DR N-PSDB; ADO39386.
 XX
 PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
 PT of a transcription factor susceptible to degradation under normoxia
 PT conditions, useful for treating anemia associated with AIDS, cancer and
 PT inflammation.
 XX
 PS Disclosure; Fig 6J; 28pp; English.
 XX
 CC The invention describes an isolated polynucleotide (1) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions; an isolated polynucleotide which codes for the chimeric
 CC transactivator (1); a vector comprising the chimeric transactivator
 CC polynucleotide (2); a composition comprising polynucleotide (2) and a
 CC polynucleotide which contains a sequence that codes for a target gene and
 CC a promoter which is regulated by the chimeric transactivator coded; a
 CC method of expressing a target gene in a subject, comprising administering
 CC the composition of (4); a method of increasing the number of red blood
 CC cells in a subject, comprising administering the composition of (4) to
 CC the subject; and a method of increasing the number of blood vessels in
 CC subject, comprising administering the composition of (4) to the subject.
 CC The methods and compositions of the present invention are useful for
 CC treating anaemia associated with AIDS or cancer, anaemia from
 CC inflammatory origin and haemoglobinopathies. This is the amino acid
 CC sequence of a fragment of a chimeric transactivator comprising regions of
 CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
 CC transcription factor gene and VP16.
 XX
 CC Sequence 632 AA;
 SQ
 Query Match 100.0%; Score 95; DB 8; Length 632;
 Best Local Similarity 94.7%; Pred. No. 3.6e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 DB 235 DLDLEMLAXYIPMDDDFQL 253
 |||||:|||||
 RESULT 41
 AAY94629
 ID AAY94629 standard; protein; 652 AA.
 XX
 AC AAY94629;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE HIF-1alpha variant protein sequence HIF-1alpha/1-652.
 XX
 KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200029437-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 11-NOV-1999; 99WO-SE002053.
 XX
 PR 13-NOV-1998; 98SE-00003891.
 XX
 PA (PHAA) PHARMACIA & UPJOHN AB.
 XX
 XX

PI Berkenstam A, Poellinger L;
 XX
 DR WPI; 2000-399715/34.
 XX
 PT Human hypoxia-inducible factor alpha variants for identifying compounds
 PT that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 XX
 PS Claim 15; Page 69-70; 87pp; English.
 XX
 CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390; a C-terminal
 CC nuclear localization sequence located at amino acids 718-584; a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584;
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of
 CC angiogenesis, erythropoiesis and glycolysis
 XX
 CC Sequence 652 AA;
 SQ
 Query Match 100.0%; Score 95; DB 3; Length 652;
 Best Local Similarity 94.7%; Pred. No. 3.7e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 DB 556 DLDLEMLAXYIPMDDDFQL 574
 |||||:|||||
 RESULT 42
 AAY84167
 ID AAY84167 standard; protein; 669 AA.
 XX
 AC AAY84167;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX
 KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 KW ischemic tissue damage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200010578-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US019416.
 XX
 PR 25-AUG-1998; 98US-00148547.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Semenza GL;
 XX
 DR WPI; 2000-246493/21.
 XX

PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
 PT treating hypoxia or ischemia-related tissue damage.
 XX
 PS Claim 1; Page; 96pp; English.
 XX
 CC The present sequence represents a variant of hypoxia-inducible factor
 CC (HIF)-1 alpha, comprising amino acids 1-391 and 549-826 of the wild type
 CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
 CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
 CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
 CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
 CC which residues 551 and 552 are not serine and threonine, respectively.
 CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
 CC expression of a hypoxia inducible gene in a cell. They are also useful for
 CC providing constitutive expression of a hypoxia inducible factor in a
 CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
 CC therapy for inducing the level of angiogenesis in tissues of patients at
 CC risk of coronary artery disease or ischemic tissue damage. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided
 XX
 SQ Sequence 669 AA;

Query Match 100.0%; Score 95; DB 3; Length 669;
 Best Local Similarity 94.7%; Pred. No. 3.8e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 DB 399 DLDLEMLAXYIPMDDDFQL 417

RESULT 43
 AAY84166
 ID AAY84166 standard; protein; 697 AA.
 XX
 AC AAY84166;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX
 KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 KW ischemic tissue damage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 422
 FT /note= "this residue is optionally not Ser, and is
 FT preferably Gly"
 FT Misc-difference 423
 FT /note= "this residue is optionally not Thr, and is
 FT preferably Ala"
 XX
 PN WO200010578-A1.

XX
 XX 02-MAR-2000.
 XX
 XX 25-AUG-1999; 99WO-US019416.
 XX
 XX 25-AUG-1999; 98US-00148547.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX Semenza GL;
 XX
 XX WPI; 2000-246493/21.

PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
 PT treating hypoxia or ischemia-related tissue damage.
 XX
 PS Claim 1; Page; 96pp; English.
 XX
 CC The present sequence represents a variant of hypoxia-inducible factor
 CC (HIF)-1 alpha, comprising amino acids 1-391 and 521-826 of the wild type
 CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
 CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
 CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
 CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
 CC which residues 551 and 552 are not serine and threonine, respectively.
 CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
 CC expression of a hypoxia inducible gene in a cell. They are also useful for
 CC providing constitutive expression of a hypoxia inducible factor in a
 CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
 CC therapy for inducing the level of angiogenesis in tissues of patients at
 CC risk of coronary artery disease or ischemic tissue damage. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided
 XX
 SQ Sequence 697 AA;

Query Match 100.0%; Score 95; DB 3; Length 697;
 Best Local Similarity 94.7%; Pred. No. 4e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
 |||||:|||||
 DB 427 DLDLEMLAXYIPMDDDFQL 445

RESULT 44
 AAY84173
 ID AAY84173 standard; protein; 701 AA.
 XX
 AC AAY84173;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE A variant of human hypoxia inducible factor-1 alpha protein.
 XX
 KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
 KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
 KW ischemia related damage; angiogenesis; coronary artery disease;
 KW ischemic tissue damage.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 426
 FT /note= "this residue is not Ser, and is preferably Gly"
 FT Misc-difference 427
 FT /note= "this residue is not Thr, and is preferably Ala"
 XX
 PN WO200010578-A1.

XX
 XX 02-MAR-2000.
 XX
 XX 25-AUG-1999; 99WO-US019416.
 XX
 XX 25-AUG-1999; 98US-00148547.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX Semenza GL;
 XX
 XX WPI; 2000-246493/21.

XX
 XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
 XX treating hypoxia or ischemia-related tissue damage.
 PT

XX PS Claim 1; Page; 96pp; English.

XX CC The present sequence represents a variant of hypoxia-inducible factor

XX CC (HIF)-1 alpha, comprising amino acids 1-391 and 517-826 of the wild type

XX CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic

XX CC and non-hypoxic conditions. The variants comprises amino acid residues 1-

XX CC 391 and 517-826 of the wild type human HIF-1alpha polypeptide, in

XX CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in

XX CC which residues 551 and 552 are not serine and threonine, respectively.

XX CC The HIF-1alpha variant polynucleotide sequences are useful for increasing

XX CC expression of a hypoxia inducible gene in a cell. They are also useful for

XX CC providing constitutive expression of a hypoxia inducible factor in a

XX CC cell, and for reducing or preventing hypoxia or ischemia related damage.

XX CC The variant HIF-1alpha polypeptides are useful for providing prophylactic

XX CC therapy for inducing the level of angiogenesis in tissues of patients at

XX CC risk of coronary artery disease or ischemic tissue damage. note: this

XX CC sequence does not appear in the specification; it was created using

XX CC information provided

XX SQ Sequence 701 AA;

Query Match 100.0%; Score 95; DB 3; Length 701;

Best Local Similarity 94.7%; Pred. No. 4e-06;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19

Db 431 DLDLEMLAPYIPMDDDFQL 449

RESULT 45

AAAY84172

ID AAY84172 standard; protein; 710 AA.

XX AC AAY84172;

XX DT 03-JUL-2000 (first entry)

XX DE A variant of human hypoxia inducible factor-1 alpha protein.

XX KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;

XX KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;

XX KW ischemia related damage; angiogenesis; coronary artery disease;

XX KW ischemic tissue damage.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 435

FT /note= "this residue is not Ser, and is preferably Gly"

FT Misc-difference 436

FT /note= "this residue is not Thr, and is preferably Ala"

FT

PN WO200010578-A1.

XX PD 02-MAR-2000.

XX PF 25-AUG-1999; 99WO-US019416.

XX PR 25-AUG-1998; 99US-00148547.

XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Semenza GL;

XX DR WPI; 2000-246493/21.

XX PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for

XX PT treating hypoxia or ischemia-related tissue damage.

XX PS Claim 1; Page; 96pp; English.

XX CC The present sequence represents a variant of hypoxia-inducible factor

XX CC (HIF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild type

XX CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic

XX CC and non-hypoxic conditions. The variants comprises amino acid residues 1-

XX CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,

XX CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in

XX CC which residues 551 and 552 are not serine and threonine, respectively.

XX CC The HIF-1alpha variant polynucleotide sequences are useful for increasing

XX CC expression of a hypoxia inducible gene in a cell. They are also useful for

XX CC providing constitutive expression of a hypoxia inducible factor in a

XX CC cell, and for reducing or preventing hypoxia or ischemia related damage.

XX CC The variant HIF-1alpha polypeptides are useful for providing prophylactic

XX CC therapy for inducing the level of angiogenesis in tissues of patients at

XX CC risk of coronary artery disease or ischemic tissue damage. note: this

XX CC sequence does not appear in the specification; it was created using

XX CC information provided

XX SQ Sequence 710 AA;

Query Match 100.0%; Score 95; DB 3; Length 710;

Best Local Similarity 94.7%; Pred. No. 4.1e-06;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19

Db 440 DLDLEMLAPYIPMDDDFQL 458

RESULT 46

AAAY84171

ID AAY84171 standard; protein; 724 AA.

XX AC AAY84171;

XX DT 03-JUL-2000 (first entry)

XX DE A variant of human hypoxia inducible factor-1 alpha protein.

XX KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;

XX KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;

XX KW ischemia related damage; angiogenesis; coronary artery disease;

XX KW ischemic tissue damage.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 449

FT /note= "this residue is not Ser, and is preferably Gly"

FT Misc-difference 450

FT /note= "this residue is not Thr, and is preferably Ala"

FT

PN WO200010578-A1.

XX PD 02-MAR-2000.

XX PF 25-AUG-1999; 99WO-US019416.

XX PR 25-AUG-1998; 98US-00148547.

XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Semenza GL;

XX DR WPI; 2000-246493/21.

XX PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for

XX PT treating hypoxia or ischemia-related tissue damage.

XX PS Claim 1; Page; 96pp; English.

XX CC The present sequence represents a variant of hypoxia-inducible factor

CC (HIF)-1 alpha, comprising amino acids 1-391 and 494-826 of the wild type protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826, 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in which residues 551 and 552 are not serine and threonine, respectively. The HIF-1alpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They are also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-1alpha polypeptides are useful for providing prophylactic therapy for inducing the level of angiogenesis in tissues of patients at risk of coronary artery disease or ischemic tissue damage. note: this sequence does not appear in the specification; it was created using information provided

XX SQ Sequence 724 AA;

Query Match 100.0%; Score 95; DB 3; Length 724;
Best Local Similarity 94.7%; Pred. No. 4.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
DB 454 DLDLEMLAPYIPMDDDFOL 472

RESULT 47
ABR82375
ID ABR82375 standard; protein; 735 AA.

XX AC ABR82375;

DT 06-NOV-2003 (first entry)

XX DE Hypoxia-inducible factor 1 (HIF-1) alpha variant sequence.

XX KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO; erythropoietin; vascular endothelial growth factor; VEGF; glycolytic; tranquilizer; vulnery; cardiant; cerebroprotective; variant.

XX OS Homo sapiens.

XX PN WO2003057820-A2.

XX PD 17-JUL-2003.

XX PF 04-OCT-2002; 2002WO-US031699.

XX PR 21-DEC-2001; 2001US-00032361.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Mcgrath K;

XX DR WPI; 2003-645988/61.

XX PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha ubiquitination, and activator of vascular endothelial growth factor transcription useful for treating tissue injuries including wounds, surgical incisions.

XX PS Disclosure; Page 5-6; 37pp; English.

XX CC The invention relates to peptide inhibitors of hypoxia-inducible factor (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the transcription of erythropoietin (EPO), vascular endothelial growth factor (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful for treating tissue injuries including wounds, surgical incisions, chronic wounds, heart disease and stroke. The present sequence represents a HIF-1 alpha variant sequence

XX SQ Sequence 735 AA;

Query Match 100.0%; Score 95; DB 6; Length 735;
Best Local Similarity 94.7%; Pred. No. 4.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
DB 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 48
ADN75066
ID ADN75066 standard; protein; 735 AA.

XX AC ADN75066;

DT 12-AUG-2004 (first entry)

XX DE Human hypoxia-inducible factor 1 alpha #2.

XX KW human; antisense therapy; hypoxia-inducible factor 1 alpha; hyperproliferative disorder.

XX OS Homo sapiens.

XX PN US2004101858-A1.

XX PD 27-MAY-2004.

XX PF 23-NOV-2002; 2002US-00304126.

XX PR 23-NOV-2002; 2002US-00304126.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Ward DT, Dobie KW;

XX DR WPI; 2004-399686/37.

XX DR N-PSDB; ADN74945.

XX PT New compounds, particularly oligonucleotides targeted to a nucleic acid encoding hypoxia-inducible factor 1 alpha, useful for treating diseases associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative disorders.

XX PS Disclosure; Page 57-59; 80pp; English.

XX CC The invention relates to antisense oligonucleotides targeted to, and which specifically hybridise with, and inhibit expression of, a nucleic acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense oligonucleotides are useful for treating a disease or condition associated with hypoxia-inducible factor 1 alpha, such as a hyperproliferative disorder. They are also useful in research and CC diagnostics for modulating the expression of hypoxia-inducible factor 1 alpha. The present sequence represents human hypoxia-inducible factor 1 alpha #2.

XX SQ Sequence 735 AA;

Query Match 100.0%; Score 95; DB 8; Length 735;
Best Local Similarity 94.7%; Pred. No. 4.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
DB 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 49
AAY84170
ID AAY84170 standard; protein; 749 AA.

XX AC AAY84170;


```
XX 03-JUL-2000 (first entry)
XX DE
XX DT
XX DE A variant of human hypoxia inducible factor-1 alpha protein.
XX KW
XX KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
XX KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
XX KW ischemia related damage; angiogenesis; coronary artery disease;
XX KW ischemic tissue damage.
XX OS
XX OS Synthetic.
XX OS Homo sapiens.
XX OS
XX FH Location/Qualifiers
XX FT Misc-difference 474
XX FT /note= "this residue is not Ser, and is preferably Gly"
XX FT Misc-difference 475
XX FT /note= "this residue is not Thr, and is preferably Ala"
XX FT
XX PN W0200010578-Al.
XX XX
XX XX 02-MAR-2000.
XX PD
XX XX 25-AUG-1999; 99WO-US019416.
XX XX
XX XX 25-AUG-1998; 98US-00148547.
XX PR
XX XX (UJVO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PA
XX PI Semenza GL;
XX DR
XX DR WPI; 2000-246493/21.
XX XX
XX FT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX FT treating hypoxia or ischemia-related tissue damage.
XX PS
XX PS Claim 1; Page; 96pp; English.
XX CC
XX CC The present sequence represents a variant of hypoxia-inducible factor
XX CC (HIF)-1 alpha, comprising amino acids 1-391 and 469-826 of the wild type
XX CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
XX CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
XX CC 391 and 531-826, 429-826, 469-826, 494-826, 508-826,
XX CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
XX CC which residues 551 and 552 are not serine and threonine, respectively.
XX CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
XX CC expression of a hypoxia inducible gene in a cell. They are also useful for
XX CC providing constitutive expression of a hypoxia inducible factor in a
XX CC cell, and for reducing or preventing hypoxia or ischemia related damage.
XX CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
XX CC therapy for inducing the level of angiogenesis in tissues of patients at
XX CC risk of coronary artery disease or ischemic tissue damage. note: this
XX CC information does not appear in the specification; it was created using
XX CC information provided
XX SQ
XX SQ Sequence 749 AA;
XX Query Match 100.0%; Score 95; DB 3; Length 749;
XX Best Local Similarity 94.7%; Pred. NO. 4.3e-06;
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDLEMLAXYIPMDDDFQL 19
XX |||||:|||||
XX Db 479 DLDLEMLAPYIPMDDDFQL 497
XX
XX RESULT 50
XX AAY94635
XX ID AAY94635 standard; protein; 756 AA.
XX AC AAY94635;
XX XX
XX DT 15-AUG-2000 (first entry)
XX
XX HIF-1alpha variant protein sequence HIF-1alpha/71-826.
XX DE
XX DT
XX KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
XX KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX OS
XX OS Homo sapiens.
XX XX
XX PN W0200029437-Al.
XX XX
XX XX 25-MAY-2000.
XX PD
XX XX 11-NOV-1999; 99WO-SE002053.
XX XX
XX PR 13-NOV-1998; 98SE-00003891.
XX XX
XX PA (PHAA ) PHARMACIA & UPJOHN AB.
XX XX
XX PI Berkenstam A, Poellinger L;
XX XX
XX DR WPI; 2000-399715/34.
XX XX
XX CC Human hypoxia-inducible factor alpha variants for identifying compounds
XX CC that modulate its functional domain and regulate genes involved in
XX CC angiogenesis, erythropoiesis.
XX FT
XX FT Claim 20; Page 79-82; 87pp; English.
XX PS
XX PS This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX CC multi-step process which includes hypoxia-dependent nuclear import and
XX CC activation of the transactivation domain. The HIF-1alpha consists of a
XX CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX CC nuclear localization sequence located at amino acids 718-584, a
XX CC transactivator domain (N-TAD) located between amino acids 531 and 584,
XX CC and a second transactivator domain (C-TAD) located between 813 and 826.
XX CC The invention relates to isolated variants of HIF-1alpha, such as that
XX CC represented by the present sequence. The variants are useful for
XX CC identifying compounds capable of modulating the function of a functional
XX CC domain of human HIF-1alpha. The method comprises contacting a candidate
XX CC compound with a cell expressing a HIF-1alpha variant conjugated to a
XX CC molecular probe. The localization of the probe can be detected in the
XX CC cell. The Aequorea victoria green fluorescent protein can be used as the
XX CC molecular probe. The compounds are useful for the regulation of HIF-
XX CC 1alpha target genes, such as those involved in the regulation of
XX CC angiogenesis, erythropoiesis an glycolysis
XX SQ
XX SQ Sequence 756 AA;
XX Query Match 100.0%; Score 95; DB 3; Length 756;
XX Best Local Similarity 94.7%; Pred. NO. 4.4e-06;
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDLEMLAXYIPMDDDFQL 19
XX |||||:|||||
XX Db 486 DLDLEMLAPYIPMDDDFQL 504
XX
XX Search completed: February 8, 2005, 20:15:09
XX Job time : 103.667 secs
```


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OM protein - protein search, using sw model

Run on: February 8, 2005, 20:05:10 ; Search time 19.6667 Seconds
(without alignments)
92.955 Million cell updates/sec

Title: US-10-032-361-5
Perfect score: 95
Sequence: 1 DLDLEMLAXYIPMDDDFQL 19

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	810	2 JC4837	hypoxia-inducible
2	95	100.0	811	2 JC7619	hypoxia-inducible
3	95	100.0	813	2 JC5809	hypoxia-inducible
4	95	100.0	826	2 I38972	hypoxia-inducible
5	81	85.3	667	2 JC7771	hypoxia-inducible
6	48	50.5	800	2 S29344	protein kinase KIN
7	48	50.5	1505	2 JC4851	hypoxia-inducible
8	47	49.5	707	1 Q9BEJ5	phosphotransferase
9	47	49.5	1866	1 C3GP	complement C3 prec
10	45	47.4	700	2 S38361	calpain (EC 3.4.22
11	45	47.4	726	2 A27602	complement C3 - ya
12	45	47.4	876	2 S62152	SFB2 protein - ya
13	44	46.3	137	2 G70090	hypothetical prote
14	44	46.3	214	2 G69380	hypothetical prote
15	44	46.3	324	2 F64144	hypothetical prote
16	44	46.3	2599	2 F90608	ABC transporter pe
17	43	45.3	310	1 S37695	calcium-binding pr
18	43	45.3	360	2 G72673	hypothetical prote
19	43	45.3	367	1 F64070	histidinol-phospha
20	43	45.3	390	2 F72863	AcOrf-109 protein
21	43	45.3	391	2 T41849	AcMNPV orf109 - Bo
22	43	45.3	865	2 S69044	hypothetical prote
23	43	45.3	1663	1 C3RT	complement C3 prec
24	42.5	44.7	415	2 B83634	hypothetical prote
25	42.5	44.7	474	2 F81283	catalase (EC 1.11.
26	42.5	44.7	507	2 I40767	catalase (EC 1.11.
27	42	44.2	235	2 G86567	lipoate-protein li
28	42	44.2	235	2 F72056	lipoate-protein li
29	42	44.2	660	2 S50383	gamma-glutamyltran

30	42	44.2	690	2 A10207	tail-specific prot
31	42	44.2	700	2 S57194	calpain (EC 3.4.22
32	42	44.2	724	1 RRMQTD	RNA-directed RNA p
33	42	44.2	1088	2 T14917	homeotic protein P
34	42	44.2	1227	2 T23004	hypothetical prote
35	42	44.2	1244	2 T19068	hypothetical prote
36	41	43.2	259	2 S32898	hypothetical prote
37	41	43.2	278	2 T02422	hypothetical prote
38	41	43.2	391	2 A57633	hypothetical prote
39	41	43.2	391	2 AD2856	conserved hypotHet
40	41	43.2	395	2 T18582	hypothetical prote
41	41	43.2	432	2 H82358	conserved hypotHet
42	41	43.2	500	2 G71633	ADP,ATP carrier pr
43	41	43.2	751	2 AG1329	penicillin-binding
44	41	43.2	752	2 AG1700	penicillin-binding
45	41	43.2	810	2 A64742	hypothetical prote
46	41	43.2	810	2 C90651	hypothetical prote
47	41	43.2	810	2 C85502	hypothetical prote
48	41	43.2	887	2 S43196	[protein-Pil] urid
49	41	43.2	898	2 S65474	pyruvate dehydroge
50	41	43.2	1009	2 S44621	C50C3.2 protein -
51	41	43.2	1215	2 S50428	probable Ca2+-tran
52	40.5	42.6	240	2 E83896	hypothetical prote
53	40.5	42.6	540	2 B96631	probable polygalac
54	40	42.1	113	2 A50629	cell invasion prot
55	40	42.1	129	2 A99399	hypothetical prote
56	40	42.1	196	2 B65207	hypothetical 22.6
57	40	42.1	196	2 B91244	hypothetical prote
58	40	42.1	196	2 H86091	hypothetical prote
59	40	42.1	196	2 A00454	conserved hypotHet
60	40	42.1	205	2 S42406	protein phosphatas
61	40	42.1	205	2 T46876	phosphoprotein pho
62	40	42.1	280	2 B45537	viral coat protein
63	40	42.1	292	2 B83690	aminoglycoside 6-a
64	40	42.1	328	2 ACl300	FtsY of E. coli an
65	40	42.1	328	2 ACl672	FtsY of E. coli an

ALIGNMENTS

RESULT 1

JC4837
hypoxia-inducible factor 1 alpha - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4837
R:Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M.
Biochem. Biophys. Res. Commun. 223, 54-59, 1996
A:Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxi
A:Reference number: JC4837; MUID:96254028; PMID:8660378
A:Accession: JC4837
A:Molecule type: mRNA
A:Residues: 1-810 <WEN>
A:Cross-references: UNIPROT:Q61221; EMBL:X95580; NID:gi430864; PIDN:CAA64833.1; PID:G437
C:Comment: This factor is involved in the oxygen-regulated transcription of several gene

C:Genetics:
A:Gene: Hif1alpha
A:Map position: 12
C:Keywords: transcription factor
F:5-58/Region: helix-loop-helix #status predicted

Query Match 100.0%; Score 95; DB 2; Length 810;
Best Local Similarity 94.7%; Pred. No. 4.7e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 543 DLDLEMLAXYIPMDDDFQL 561

RESULT 2

JC7619

hypoxia-inducible factor 1 alpha - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: J07619
R:Kobayashi, T.; Sugishita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kinugawa, K.; Harada, R.
Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001
A:Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventricle
A:Reference number: J07619; MUID:21134360; PMID:11237772
A:Contents: Embryonic ventricular myocytes
A:Accession: J07619
A:Molecule type: mRNA
A:Residues: 1-811 <TAK>
A:Cross-references: DBJ:AB013746
A:Comment: This factor belongs to the basic helix-loop-helix-Per/ARNT/Sim (HLH-PAS) family of transcription factors, and in redox stimuli.
C:Genetics:
A:Gene: hif-1alpha
C:Keywords: embryo; transcription factor
F:106-156/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS1>
F:249-299/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS2>
F:762-811/Domain: conserved carboxy-terminal transactivation element #status predicted <PAS3>
F:767-768/Region: conserved dileucine repeat, important for oxygen-dependent degradation

Query Match 100.0%; Score 95; DB 2; Length 811;
Best Local Similarity 94.7%; Pred. No. 4.7e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 554 DLDLEMLAPYIPMDDDFQL 572

RESULT 3
JC5809
hypoxia-inducible factor 1 alpha - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999
C:Accession: JC5809
R:Ladoux, A.; Prelin, C.
Biochem. Biophys. Res. Commun. 240, 552-556, 1997
A:Title: Cardiac expressions of Hif-1 alpha and HLF/EPAS, two basic loop helix/PAS domain proteins, in the heart of the rat.
A:Reference number: JC5809; MUID:98063274; PMID:9398602
A:Accession: JC5809
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-813 <LAD>
C:Comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, and FGF-14/Region: basic helix-loop-helix #status predicted

Query Match 100.0%; Score 95; DB 2; Length 813;
Best Local Similarity 94.7%; Pred. No. 4.7e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 543 DLDLEMLAPYIPMDDDFQL 561

RESULT 4
I38972
hypoxia-inducible factor 1 alpha - human
N:Alternate names: ARNT interacting protein
C:Species: Homo sapiens (man)
C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: I38972; G01875
R:Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995
A:Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulating gene expression by oxygen-dependent DNA methylation
A:Reference number: I38972; MUID:95296340; PMID:7539918
A:Accession: I38972
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-826 <RES>
A:Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:G881345; PIDN:AAC50152.1; PID:G881345
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Hogensch, J.B.; Chan, W.K.; Carver, L.A.; Bradford, C.A.
submitted to the EMBL Data Library, June 1995
A:Reference number: H00692
A:Accession: G01875
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-826 <HOG>
A:Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1; PID:g1144013
C:Genetics:
A:Gene: GDB:HIF1A
A:Cross-references: GDB:512229
A:Map position: 14q21-14q24
C:Keywords: heterodimer

Query Match 100.0%; Score 95; DB 2; Length 826;
Best Local Similarity 94.7%; Pred. No. 4.8e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 5
JC7771
hypoxia inducible factor-3 alpha - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7771
R:Hara, S.; Hamada, J.; Kobayashi, C.; Kondo, Y.; Imura, N.
Biochem. Biophys. Res. Commun. 287, 808-813, 2001
A:Title: Expression and characterization of hypoxia-inducible factor (HIF)-3alpha in human cells.
A:Reference number: JC7771; PMID:11573933
A:Contents: Kidney
A:Accession: JC7771
A:Molecule type: mRNA
A:Residues: 1-667 <HAR>
A:Cross-references: UNIPROT:Q9Y2N7; DBJ:AB054067
C:Comment: This protein is a heterodimeric transcription factor that belongs to the basic-helix-loop-helix-PAS family and is involved in the regulation of hypoxia-inducible gene expression in human kidney.
C:Genetics:
A:Gene: hif-3alpha
A:Map position: 19
C:Keywords: kidney

Query Match 85.3%; Score 81; DB 2; Length 667;
Best Local Similarity 88.9%; Pred. No. 6.7e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 483 LDLEMLAPYISMDDDFQL 500

RESULT 6
S29344
protein kinase KIN3 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O5220; protein YOR233W
C:Species: Saccharomyces cerevisiae
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C:Accession: S29344; S6126; S24707
R:Kambouris, N.G.; Burke, D.J.; Creutz, C.E.
Yeast 9, 141-150, 1993
A:Title: Cloning and genetic analysis of the gene encoding a new protein kinase in Saccharomyces cerevisiae
A:Reference number: S29344; MUID:93220392; PMID:8465601
A:Accession: S29344
A:Molecule type: DNA
A:Residues: 1-800 <KAM>
A:Cross-references: UNIPROT:Q01919; EMBL:X67916; NID:G5514; PIDN:CAA48115.1; PID:G5515
R:Boyer, J.; Fairhead, C.; Gaillon, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon, B.

submitted to the Protein Sequence Database, July 1996
A:Reference number: S67104
A:Accession: S67126
A:Molecule type: DNA
A:Residues: 1-800 <BOY>
A:Cross-references: EMBL:275141; NID:g1420534; PIDN:CAA99453.1; PID:e252094; PID:g142053
A:Experimental source: strain S288C

C:Genetics:
A:Gene: SGD:KIN4; KIN3; KIN31
A:Cross-references: SGD:S0005759; MIPS:YOR233W
A:Map position: 15R
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:44-313/Domain: protein kinase homology <KIN>
F:52-60/Region: protein kinase ATP-binding motif

Query Match 50.5%; Score 48; DB 2; Length 800;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDDFQ 18
|||:|:|:|:|:
DB 245 MLAGYLPWDDHDE 257

RESULT 7

JC4851
hypoxia-inducible factor 1 alpha homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
A:Accession: JC4851
R:Nambu, J.R.; Chen, W.; Hu, S.; Crews, S.T.
Gene 172, 249-254, 1996
A:Title: The Drosophila melanogaster similar bHLH-PAS gene encodes a protein related to
A:Reference number: JC4851; MUID:96269413; PMID:8682312
A:Accession: JC4851
A:Molecule type: mRNA
A:Residues: 1-1505 <NAM>
A:Cross-references: UNIPROT:Q24167; GB:U43090; NID:g1174073; PIDN:AAC47303.1; PID:g11740
C:Genetics:
A:Gene: sima
A:Cross-references: FlyBase:FBgn0015542
A:Map position: 3
F:72-125/Region: helix-loop-helix #status predicted
F:171-433/Region: PAS domain #status predicted
F:506-635/Region: proline-rich

Query Match 50.5%; Score 48; DB 2; Length 1505;
Best Local Similarity 64.3%; Pred. No. 35;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDDFQL 19
|||:|:|:|:|:
DB 850 MRPAYIPIDDDMPL 863

RESULT 8

QOBE35
phosphotransferase (EC 2.7.1.-) - human cytomegalovirus (strain AD169)
N:Alternate names: HSRF3 protein
C:Species: human cytomegalovirus, human herpesvirus 5
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
A:Accession: S09862
R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrall, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A:Reference number: S09749; MUID:90269039; PMID:2161319
A:Accession: S09862
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-707 <CHE>

A:Cross-references: UNIPROT:P16788; EMBL:X17403; NID:g59591; PIDN:CAA35333.1; PID:g17808
A:Note: possible protein-coding frames are given
A:Note: the DNA sequence was submitted to EMBL, December 1989, in computer-readable form
C:Superfamily: human cytomegalovirus phosphotransferase
C:Keywords: phosphotransferase

Query Match 49.5%; Score 47; DB 1; Length 707;
Best Local Similarity 41.2%; Pred. No. 21;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDF 17
:|:|:|:|:|:|:
DB 304 ELSISYLLVYVPKEDDF 320

RESULT 9

C3GP
complement C3 precursor - guinea pig
N:Contains: alternative-complement-pathway C3/C5 convertase (SC 3.4.21.47) C3b subunit;
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-Feb-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
A:Accession: A37156; S03375; A20342; D20342; C20342; A31222
R:Auerbach, H.S.; Burger, R.; Dodds, A.; Colten, H.R.
J. Clin. Invest. 86, 96-106, 1990
A:Title: Molecular basis of complement C3 deficiency in guinea pigs.
A:Reference number: A37156; MUID:90307998; PMID:1973176
A:Accession: A37156
A:Molecule type: mRNA
A:Residues: 1-1666 <AUE>
A:Cross-references: UNIPROT:P12387; GB:M34054; NID:g191262; PIDN:AAA37038.1; PID:g305333
R:Gerard, N.P.; Lively, M.O.; Gerard, C.
Protein Seq. Data Anal. 1, 473-478, 1988
A:Title: Amino acid sequence of guinea pig C3a anaphylatoxin.
A:Reference number: S03375; MUID:89113342; PMID:3064079
A:Accession: S03375
A:Molecule type: protein
A:Residues: 676-730, 'N', 732-752 <GER>
A:Experimental source: complement-activated guinea pig serum
A:Note: form isolated is inactive C3a anaphylatoxin and is missing the carboxyl-terminal
R:Thomas, M.L.; Tack, B.F.
Biochemistry 22, 942-947, 1983
A:Title: Identification and alignment of a thiol ester site in the third component of gu
A:Reference number: A90479; MUID:83178889; PMID:6838833
A:Accession: A20342
A:Molecule type: protein
A:Residues: 676-687 <TH1>
A:Accession: D20342
A:Molecule type: protein
A:Residues: 993-1012, 1014-1017, 'E', 1019-1030, 'Y' <TH2>
R:Goldberger, G.; Thomas, M.L.; Tack, B.F.; Williams, J.; Colten, H.R.; Abraham, G.N.
J. Biol. Chem. 256, 12617-12619, 1981
A:Title: NH2-terminal structure and cleavage of guinea pig pro-C3, the precursor of the
A:Reference number: A20342; MUID:82075767; PMID:6458605
A:Accession: C20342
A:Molecule type: protein
A:Residues: 23-38 <GOL>
C:Comment: Complement C3 contains two chains, formed by removal of four residues and lin
native-complement-pathway C3/C5 convertase.
C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C:Comment: The major site of synthesis of this plasma protein is the liver.
C:Superfamily: alpha-2-macroglobulin
C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein.
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-671/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F:23-671, 676-1666/Product: complement C3 #status predicted <C3>
F:23-671, 754-1666/Product: complement C3b #status predicted <C3B>
F:676-1666/Product: complement C3 alpha chain #status predicted <C3A>
F:676-753/Product: C3a anaphylatoxin #status predicted <C3r>
F:754-1666/Product: complement C3b alpha chain #status predicted <C3BA>
F:951-1308/Product: C3dk fragment #status predicted <CDK>

3

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LEMLXYPMDDD 16
:|:|:|:|
Db 34 IENLIVVPTDDD 46

RESULT 22
S69044
hypothetical protein YPL414c - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein LPI5
C:Species: *Saccharomyces cerevisiae*
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004
A:Accession: S69044
R:Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.;
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of *Saccharomyces cerevisiae* chromosome XVI left arm.
A:Reference number: S69040
A:Accession: S69044
A:Molecule type: DNA
A:Residues: 1-865 <HAL>
A:Cross-references: UNIPROT:Q03002; EMBL:U43703; NID:G1244769; PIDN:AAB68219.1; PID:G1244769
C:Genetics:
A:Cross-references: SGD:S0006062
A:Map position: 16L
A:Note: YPL414c
C:Superfamily: protein kinase homology
C:Keywords: ATP
F:39-313/Domain: protein kinase homology <KIN>
F:47-55/Region: protein kinase ATP-binding motif

Query Match 45.3%; Score 43; DB 2; Length 865;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 MLXLYPMDDD 16
:|:|:|:|
Db 245 ILAGLYPMDDD 255

RESULT 23
C3RT
complement C3 precursor - rat
N:Alternate names: 37K phospholipase A2 inhibitory protein
N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C:Species: *Rattus norvegicus* (Norway rat)
C>Date: 04-Dec-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
A:Accession: S15764; A54562; A01260; B35979; A35979; PNO567; A32281; S08692
R:Misumi, Y.; Sohda, M.; Ikehara, Y.
Nucleic Acids Res. 18, 2178, 1990
A:Title: Nucleotide and deduced amino acid sequence of rat complement C3.
A:Reference number: S15764; MUID:90245672; PMID:2336397
A:Accession: S15764
A:Molecule type: mRNA
A:Residues: 1-1663 <MIS>
A:Cross-references: UNIPROT:P01026; EMBL:X52477; NID:G56953; PIDN:CAA36716.1; PID:G56954
R:Sundstrom, S.A.; Komm, B.S.; Ponce-de-Leon, H.; Yi, Z.; Teuscher, C.; Lyttle, C.R.
J. Biol. Chem. 264, 16941-16947, 1989
A:Title: Estrogen regulation of tissue-specific expression of complement C3.
A:Reference number: A54562; MUID:89380332; PMID:2674144
A:Accession: A54562
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 'P', 1316-1595 <SUN>
A:Cross-references: GB:M9866; NID:G203200; PIDN:AAA40837.1; PID:G554423
R:Jacobs, J.W.; Rubin, J.S.; Hugli, T.E.; Bogardt, R.A.; Mariz, I.K.; Daniels, J.S.; Dau
Biochemistry 17, 5031-5038, 1978
A:Title: Purification, characterization, and amino acid sequence of rat anaphylatoxin (C3a).
A:Reference number: A01260; MUID:79062262; PMID:309768
A:Accession: A01260
A:Molecule type: protein
A:Residues: 671-703, 'K', 705-720, 'KL', 723-748 <JAC>
A:Note: three disulfide bonds are present

R:Suwa, Y.; Kudo, I.; Imizumi, A.; Okada, M.; Kamimura, T.; Suzuki, Y.; Chang, H.W.; Ha
Proc. Natl. Acad. Sci. U.S.A. 87, 2395-2399, 1990
A:Title: Proteinaceous inhibitors of phospholipase A-2 purified from inflammatory sites
A:Reference number: A35979; MUID:90207203; PMID:2320562
A:Accession: B35979
A:Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 998-1005 <SUM>
A:Accession: A35979
A:Molecule type: protein
A:Residues: 'X', 961-962, 'P', 964-969 <SU2>
R:Nakagawa, H.; Komorita, N.
Biochem. Biophys. Res. Commun. 194, 1181-1187, 1993
A:Title: Complement component C3-derived neutrophil chemotactic factors purified from ex
A:Reference number: PNO566; MUID:93356786; PMID:8352775
A:Accession: PNO567
A:Molecule type: protein
A:Residues: 568-592 <NAK>
A:Note: amino end of a C3-derived peptide designated exudate neutrophil chemotactic fact
A:Accession: PNO566
A:Molecule type: protein
A:Residues: 671-687 <NA2>
A:Note: amino end of peptide designated neutrophil chemotactic factor 1 and probably ide
R:Kuivaniemi, P.C.; Capulong, R.B.; Harkins, R.N.; DeSombre, E.R.
Biochem. Biophys. Res. Commun. 158, 898-905, 1989
A:Title: The estrogen-responsive 110K and 74K rat uterine secretory proteins are structu
A:Reference number: A32281; MUID:89149812; PMID:2645873
A:Accession: A32281
A:Molecule type: protein
A:Residues: 25-41 <KUI>
A:Experimental source: 17beta-estradiol-stimulated uterus of immature rat
A:Note: The authors treat this 74K uterine secretory protein, identical as far as sequen
ent
C:Comment: Complement C3 contains two chains, formed by removal of four residues and lin
alternative-complement-pathway C3/C5 convertase.
C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C:Comment: The major site of synthesis of this plasma protein is the liver.
C:Superfamily: alpha-2-macroglobulin
C:Keywords: acute phase; chemotaxis; complement alternate pathway; complement pathway; C
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-666/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F:25-666, 671-1663/Product: complement C3 #status predicted <CC3>
F:25-666, 749-1663/Product: complement C3b #status predicted <C3B>
F:671-1663/Product: complement C3 alpha chain #status predicted <CC3A>
F:671-748/Product: C3a anaphylatoxin #status experimental <C3T>
F:749-1663/Product: complement C3b alpha' chain #status predicted <C3BA>
F:946-1303/Product: C3dk fragment #status predicted <CDK>
F:1002-1303/Product: C3d fragment #status predicted <CDK>
F:1424-1457/Region: properdin binding
F:558-816, 826-861, 693-720, 694-727, 707-728, 873-1513, 1101-1158, 1358-1489, 1389-1458, 1506-15
F:748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F:939, 1617/Binding site: carboxylate (Asn) (covalent) #status predicted
F:1010-1013/Cross-link: thiolester (Cys-Gln) #status predicted
F:1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F:1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted

A/Accession: 1-235 <ARN>
A/Cross-references: UNIPROT:Q977T6; GB:AE001646; GB:AE001363; NID:94376910; PIDN:AAD1875
A/Experimental source: strain CWL029
A/Read: T.D.; Brunham, R.C.; Shen, C.; Gail, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: BA1500. MIMD-20150255. PWD1:106484915

A:Accession: C81610
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <REA>
A:Cross-References: GB:AE002174; GB:AE002161; NID:g7189059; PIDN:AAF38012.1; PID:g718906
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: lplA_2; CP0129

Query Match 44.2%; Score 42; DB 2; Length 235;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDLEMLAXYIPM 13
|:|:|:|:|:|:
DB 155 DIDLDKLSYLP 167

RESULT 29
S50383
gamma-glutamyltransferase homolog YLR299w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L8003.4
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50383

R:Pauley, A.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 8003.
A:Reference number: S50366

A:Accession: S50383
A:Molecule type: DNA
A:Residues: 1-660 <PAU>
A:Cross-References: UNIPROT:Q05902; EMBL:U17243; NID:g596030; PIDN:AAB67344.1; PID:g5960

C:Genetics:
A:Gene: SGD:ECM38
A:Cross-References: SGD:S0004290; MIPS:YLR299w
A:Map position: 12R
C:Superfamily: gamma-glutamyltransferase
C:Keywords: transmembrane protein
F:14-30/Domain: transmembrane #status predicted <TMM>

Query Match 44.2%; Score 42; DB 2; Length 660;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLEMLAXYIPMDD 16
|:|:|:|:|:|:
DB 60 DVDIIAEVLKDD 73

RESULT 30
A10207
tail-specific proteinase precursor (EC 3.4.21.-) [imported] - Yersinia pestis (strain CO
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: A10207
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10207
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-690 <KUR>
A:Cross-References: UNIPROT:Q8ZFJ8; GB:AL590842; PIDN:CAC90525.1; PID:g15979736; GSPDB:G
C:Genetics:
A:Gene: YPO1705
C:Keywords: hydrolase; serine proteinase

Query Match 44.2%; Score 42; DB 2; Length 690;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 2 LDLEMLAXYIPMDDDFQL 19
|:|:|:|:|:|:
DB 242 LSLEGIGAVLQWDDDYTL 259

RESULT 31
S57194
calpain (EC 3.4.22.17) large chain 2 - chicken
N:Alternate names: m-calpain heavy chain
C:Species: Gallus gallus (chicken)
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57194
R:Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ishiura, S.; Suzuki, K.
Biochim. Biophys. Acta 1261, 381-393, 1995
A:Title: Identification of a third ubiquitous calpain species - chicken muscle express

A:Reference number: S57194; MUID:95260862; PMID:7742367
A:Accession: S57194
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-700 <SOR>

A:Cross-References: UNIPROT:Q92178; EMBL:D38026; NID:g882068; PIDN:BAA07228.1; PID:g8820
C:Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain
C:Keywords: cysteine proteinase; EF hand; hydrolase
F:75-327/Domain: calpain catalytic domain homology <CALP>
F:525-560/Domain: calmodulin repeat homology <EF1>
F:572-604/Domain: calmodulin repeat homology <EF2>
F:605-634/Domain: calmodulin repeat homology <EF3>
F:637-669/Domain: calmodulin repeat homology <EF4>
F:670-700/Domain: calmodulin repeat homology <EF5>
F:105,262,286/Active site: Cys, His, Asn #status predicted

Query Match 44.2%; Score 42; DB 2; Length 700;
Best Local Similarity 47.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LDLEMLAXYIPMDDDFQ 18
|:|:|:|:|:|:
DB 116 LNEELARVVRDQSFQ 132

RESULT 32
RWQTD
RNA-directed RNA polymerase (EC 2.7.7.48) - tobacco necrosis virus (strain D)
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: 22K protein
C:Species: tobacco necrosis virus, TNV
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JU0368
R:Coutts, R.H.A.; Rigden, J.E.; Slabas, A.R.; Lomonossoff, G.P.; Wise, P.J.
J. Gen. Virol. 72, 1521-1529, 1991
A:Title: The complete sequence of tobacco necrosis virus strain D.
A:Reference number: JU0368; MUID:91311404; PMID:1858691

A:Accession: JU0368
A:Molecule type: Genomic RNA
A:Residues: 1-724 <COU>

A:Cross-References: UNIPROT:P27209; GB:D00942
A:Note: readthrough of the terminator TAG occurs between codons AAA for 202-Lys and GGA
C:Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwarf
C:Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication
F:1-202/Product: 22K protein #status predicted <KPT>
F:427-597/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BYD>

Query Match 44.2%; Score 42; DB 1; Length 724;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LEMLAXYIPMDDDF 17
|:|:|:|:|:|:
DB 165 LAVAACFPLDSDF 178

RESULT 33
T14917
homeotic protein PRHP - parsley
N:Alternate names: homeodomain protein PRHP
C:Species: Petroselinum crispum (parsley)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14917
R:Korfage, U.; Trezzini, G.F.; Meier, I.; Hahlbrock, K.; Somasich, I.E.
Plant Cell 6, 695-708, 1994
A>Title: Plant homeodomain protein involved in transcriptional regulation of a pathogen
A:Reference number: Z16417; MUID:94312876; PMID:7913642
A:Accession: T14917
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1088 <KOR>
A:Cross-references: UNIPROT:P48786; EMBL:L21975; NID:G507797; PIDN:AAA62237.1; PID:G6661
C:Genetics:
A:Gene: PRHP
C:Function:
A:Description: binds specifically to pr2 gene promoter; transcriptional regulator
C:Keywords: DNA binding; homeobox

Query Match 44.2%; Score 42; DB 2; Length 1088;
Best Local Similarity 53.3%; Pred. NO. 2.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LDLEMLAXYIPMDDDD 16
||:|:|||||:
Db 611 LDPLLKEYIPDDDE 625

RESULT 34
T23004
hypothetical protein F59F3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23004
R:Kershaw, J.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19651
A:Accession: T23004
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1227 <WIL>
A:Cross-references: UNIPROT:Q21038; EMBL:Z68005; PIDN:CAA91990.1; GSPDB:GN000028; CESP:F59F3
A:Experimental source: clone F59F3
C:Genetics:
A:Gene: CESP:F59F3.1
A:Map position: X
A:Introns: 31/3; 58/1; 279/3; 429/2; 544/3; 638/2; 801/2; 887/1; 929/2; 1025/3; 1062/2;

Query Match 44.2%; Score 42; DB 2; Length 1227;
Best Local Similarity 31.6%; Pred. NO. 2.5e+02;
Matches 6; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFOL 19
||:|:|||||:
Db 824 DLPVEERYIYLPYNDYEI 842

RESULT 35
T19068
hypothetical protein C08B11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19068
R:Sims, M.
submitted to the EMBL Data Library, November 1994
A:Reference number: Z19069
A:Accession: T19068
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1244 <WIL>

A:Cross-references: UNIPROT:Q09441; EMBL:Z46676; PIDN:CAA86663.1; GSPDB:GN000020; CESP:CO
A:Experimental source: clone C08B11.
C:Genetics:
A:Gene: CESP:C08B11.3
A:Map position: 2
A:Introns: 225/1; 351/3; 737/2; 793/3; 836/3; 1097/2; 1202/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C08B11.3

Query Match 44.2%; Score 42; DB 2; Length 1244;
Best Local Similarity 56.2%; Pred. NO. 2.6e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LDLEMLAXYIPMDDDF 17
||:|:|||||:
Db 263 LDREIEAEYIDDDQF 278

RESULT 36
S32898
hypothetical protein 11 - Salmonella typhimurium
C:Species: Salmonella typhimurium
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S32898
R:Friedrich, M.J.; Kinsey, N.E.; Vila, J.; Kadner, R.J.
Mol. Microbiol. 8, 543-558, 1993
A>Title: Nucleotide sequence of a 13.9kb segment of the 90kb virulence plasmid of Salmon
A:Reference number: S32886; MUID:93316852; PMID:8100983
A:Accession: S32898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <FRI>
A:Cross-references: UNIPROT:Q04819; EMBL:L08613; NID:G154239; PIDN:AAC36969.1; PID:G1542

Query Match 43.2%; Score 41; DB 2; Length 259;
Best Local Similarity 53.8%; Pred. NO. 61;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LDLEMLAXYIPMD 14
||:|:|||||:
Db 65 LDVDVLKFYIPKD 77

RESULT 37
T02422
hypothetical protein At2g23690 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F27L4.13
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T02422; G84627
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.
A:Reference number: Z14658
A:Accession: T02422
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-278 <ROI>
A:Cross-references: UNIPROT:O64833; EMBL:AC004482; NID:G3152602; PIDN:AAC17093.1; PID:G3
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84627
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <STO>
A:Cross-references: GB:AE002093; NID:G3152614; PIDN:AAC17093.1; GSPDB:GN00139
C:Genetics:
A:Gene: F27L4.13; At2g23690
A:Map position: 2
A:Introns: 159/1; 213/2

Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: C85502
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-810 <STO>
 A;Cross-references: UNIPROT:P39170; GB:AE005174; NID:gl2512902; PIDN:AAG54479.1; GSPDB:G
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 C;Gene: YaeT
 C;Superfamily: protective surface antigen D-15

Query Match 43.2%; Score 41; DB 2; Length 810;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AXVIPMDD 16
 |::|::|
 Db 616 ATYVPIDD 624

RESULT 48
 S43196
 [protein-Pil] uridylyltransferase (EC 2.7.7.59) - Klebsiella pneumoniae
 N;Alternate names: Pil-uridylyltransferase
 C;Species: Klebsiella pneumoniae
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S54756; S43196
 R;Edwards, R.; Merrick, M.
 Mol. Gen. Genet. 247, 189-198, 1995
 A>Title: The role of uridylyltransferase in the control of Klebsiella pneumoniae nif gen
 A;Reference number: S54755; MUID:95272528; PMID:7753028
 A;Accession: S54756
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-887 <ED2>
 A;Cross-references: UNIPROT:P41193; EMBL:X78695; NID:g470138; PIDN:CAA55353.1; PID:g4701
 C;Genetics:
 A;Gene: glnd
 C;Superfamily: UTP-GLNB (protein Pil) uridylyltransferase
 C;Keywords: nucleotidyltransferase

Query Match 43.2%; Score 41; DB 2; Length 887;
 Best Local Similarity 87.5%; Pred. No. 2.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PMDDDFQL 19
 |::|::|
 Db 346 PIDDDFQL 353

RESULT 49
 S65474
 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) pdhE - Alcaligenes eutrophus
 C;Species: Alcaligenes eutrophus
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S65474
 R;Hein, S.; Steinbuechel, A.
 Eur. J. Biochem. 237, 674-684, 1996
 A>Title: Alcaligenes eutrophus possesses a second pyruvate dehydrogenase (E1).
 A;Reference number: S65473; MUID:96235232; PMID:8647112
 A;Accession: S65474
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-898 <HE1>
 A;Cross-references: UNIPROT:Q59107; EMBL:X91878; NID:gl272512; PIDN:CAAG2985.1; PID:gl27
 C;Genetics:
 A;Gene: pdhE
 C;Superfamily: pyruvate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain
 C;Keywords: oxidoreductase; thiamin pyrophosphate
 F;231-279/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 43.2%; Score 41; DB 2; Length 898;
 Best Local Similarity 42.1%; Pred. No. 2.5e+02;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
 |::|::|
 Db 442 DEDLESFMRFPARSDASL 460

RESULT 50
 S44621
 CS0C3.2 protein - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
 C;Accession: S44621
 R;Du, Z.
 submitted to the EMBL Data Library, May 1993
 A;Description: Sequence of the C. elegans cosmid CS0C3.
 A;Reference number: S44626
 A;Accession: S44621
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1009 <PAV>
 A;Cross-references: EMBL:L14433; NID:g289649; PIDN:AAA27973.1; PID:g289654
 C;Genetics:
 A;Introns: 290/2; 388/3; 593/3; 832/3; 871/2; 913/3; 964/3
 C;Superfamily: calmodulin repeat homology
 C;Keywords: EF hand
 F;818-850/Domain: calmodulin repeat homology <EF1>

Query Match 43.2%; Score 41; DB 2; Length 1009;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LEMLAXYIPMDDDFQL 19
 |::|::|
 Db 572 LDLLAEKIAVDKPKL 587

Search completed: February 8, 2005, 20:32:28
 Job time : 21.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 50.3333 Seconds
(without alignments)
193.301 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 101

Sequence: 1 DLDLEMLAPYIPMDDFQL 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

: Listing first 65 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	766	1 HIFA_ONCMY	Q98aw2 oncorhynchu
2	101	100.0	774	2 Q6STN7	Q6stn7 ctenopharyn
3	101	100.0	777	2 Q6EH14	Q6eh14 brachydanio
4	101	100.0	786	2 Q6SL11	Q6sl11 canis famil
5	101	100.0	802	2 Q6PI54	Q6pi54 xenopus lae
6	101	100.0	805	1 HIFA_XENLA	Q918a9 xenopus lae
7	101	100.0	811	1 HIFA_CHICK	Q9y1b9 gallus gall
8	101	100.0	819	2 Q7YSE5	Q7yse5 oryctolagus
9	101	100.0	821	2 Q6AF54	Q6af54 spermophilu
10	101	100.0	823	1 HIFA_BOVIN	Q9xta5 bos taurus
11	101	100.0	823	2 Q6IV47	Q6iv47 bos mutus g
12	101	100.0	824	2 Q6H8T3	Q6h8t3 spalax juda
13	101	100.0	825	1 HIFA_RAT	Q35800 rattus norv
14	101	100.0	826	1 HIFA_HUMAN	Q16665 homo sapien
15	101	100.0	836	1 HIFA_MOUSE	Q61221 mus musculu
16	87	86.1	630	2 Q9X54	Q9qx54 mus musculu
17	87	86.1	632	2 Q8WX1	Q8wx1 homo sapien
18	87	86.1	648	2 Q9HA12	Q9hai2 homo sapien
19	87	86.1	662	2 Q9Z215	Q9z215 mus musculu
20	87	86.1	667	2 Q9Y2N7	Q9y2n7 homo sapien
21	87	86.1	669	2 Q6K72	Q6k72 homo sapien
22	86	85.1	571	2 Q7T2E4	Q7t2e4 brachydanio
23	86	85.1	626	2 Q6EGR9	Q6egr9 brachydanio
24	86	85.1	643	2 Q6STN6	Q6stn6 ctenopharyn
25	83	82.2	662	2 Q9JHS2	Q9jhs2 rattus norv
26	80.5	79.7	835	2 Q696W2	Q696w2 ctenopharyn
27	80.5	79.7	859	2 Q6GQ12	Q6gq12 xenopus lae
28	80.5	79.7	862	2 Q6GZ61	Q6gz61 xenopus tro
29	80.5	79.7	862	2 Q6GF97	Q6gf97 xenopus lae
30	80.5	79.7	873	2 Q8QGM4	Q8qgm4 fundulus he
31	80	79.2	632	2 Q96K34	Q96k34 homo sapien

ALIGNMENTS

RESULT 1

HIFA_ONCMY
ID HIFA_ONCMY STANDARD; PRT; 766 AA.

AC Q98SW2; 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).

GN Name=HIF1A; Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=21282949; PubMed=11278461; DOI=10.1074/jbc.M009057200;

RX Soitamo A.J., Rabergh C.M.I., Gassmann M., Sistonen L., Nikunmaa M.;

RA "Characterization of a hypoxia-inducible factor (HIF-1 alpha) from

RT rainbow trout: accumulation of protein occurs at normal venous oxygen

RT tension."

RL J. Biol. Chem. 276:19699-19705(2001).

CC -!- FUNCTION: Functions as a master transcriptional regulator of the

CC adaptive response to hypoxia. Binds to core DNA sequence 5'-

CC [AG]CTG-3' within the hypoxia response element (HRE) of target

CC gene promoters. Activation requires recruitment of transcriptional

CC coactivators (By similarity).

CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an

CC alpha and a beta/ARNT subunit (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear

CC translocation in response to hypoxia (By similarity).

CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

Q6ryd1 sus scrofa
Q6ryd0 ovis aries
Q9w7c6 gallus gall
Q981a4 homo sapien
Q9xta4 bos taurus
Q9ptb3 coturnix co
P97481 mus musculu
Q97hs1 rattus norv
Q6peu2 mus musculu
Q8ggi5 fundulus he
Q24167 drosophila
Q819f9 arabidopsis
Q8gwa6 arabidopsis
Q91k13 arabidopsis
Q9agm7 legionella
Q935t8 streptococc
Q70ca8 streptococc
Q85306 salmonella
Q30917 salmonella
Q827r2 salmonella
P32479 saccharomyc
Q6ueb6 rattus norv
Q13017 homo sapien
P97393 mus musculu
Q6a9a1 propionibac
Q8jy74 bacterioph
Q8j2m8 colletotric
Q72993 schizosacch
Q01919 saccharomyc
Q6bif6 debaryomyce
Q6btq3 debaryomyce
Q7af3d neurospora
P17795 agrobacteri
Q7dkc8 agrobacteri

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or send an email to license@isb-sib.ch).
-----
DR EMBL; AF304864; AAK30364.1; --
DR HSRP; Q16665; IH2K.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
DR Activator; DNA-binding; Nuclear protein; Repeat;
KW Transcription regulation.
FT DOMAIN 718 721 Nuclear localization signal (Potential).
FT DNA_BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 82 159 PAS 1.
FT DOMAIN 230 300 PAS 2.
FT DOMAIN 304 347 PAC.
FT DOMAIN 368 373 Poly-Glu.
SQ SEQUENCE 766 AA; 85049 MW; FC25A4984104DASB CRC64;

Query Match 100.0%; Score 101; DB 1; Length 766;
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDEMLAPYIPMDDDFQL 19
Db 551 DLDEMLAPYIPMDDDFQL 569

RESULT 2
Q6STN7 PRELIMINARY; PRT; 774 AA.
AC Q6STN7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-1alpha.
GN Name=hif-1alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY450269; AAR95697.2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Q6STN7 PRELIMINARY; PRT; 774 AA.
AC Q6STN7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-1alpha.
GN Name=hif-1alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY450269; AAR95697.2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

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DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 774 AA; 85741 MW; 15BD0B2F90C611C6 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDEMLAPYIPMDDDFQL 19
Db 547 DLDEMLAPYIPMDDDFQL 565

RESULT 3
Q6EH14 PRELIMINARY; PRT; 777 AA.
AC Q6EH14;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypoxia-inducible factor 1 alpha.
GN Name=hif1a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Huang C.-R., Tsai Y.-C., Young H.-W., Wang W.-D., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY326951; AAQ91619.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 777 AA; 85897 MW; A9AFE2D2732C7A33 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 777;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDEMLAPYIPMDDDFQL 19
Db 549 DLDEMLAPYIPMDDDFQL 567

RESULT 4
Q6SL11 PRELIMINARY; PRT; 786 AA.
AC Q6SL11;

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DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor 1 alpha subunit (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Spee B., Penning L.C., Rothuizen J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY45802; AAR19225.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; HypoxindFIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
FT NON_TER 1 786
FT 786
SQ SEQUENCE 786 AA; 88015 MW; C37A27C25C343CDC CRC64;
Query Match 100.0%; Score 101; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 536 DLDLEMLAPYIPMDDDFQL 554
RESULT 5
Q6PT154
ID Q6PT154 PRELIMINARY; PRT; 802 AA.
AC Q6PT154;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hif1a-prov protein.
OS xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strauberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC043769; AAH43769.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; HypoxindFIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 802 AA; 90177 MW; 30A571277A9A5B1F CRC64;
Query Match 100.0%; Score 101; DB 2; Length 802;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 550 DLDLEMLAPYIPMDDDFQL 568
RESULT 6
HIFA_XENLA
ID HIFA_XENLA STANDARD; PRT; 805 AA.
AC Q918A3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIFA;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kietzmann T.;
RT "Cloning and expression of the Xenopus laevis hypoxia inducible factor
1 alpha homologue";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
adaptive response to hypoxia. Binds to core DNA sequence 5'-

```

CC CC [AG]CTGTG-3' within the hypoxia response element (HRE) of target
CC CC gene promoters. Activation requires recruitment of transcriptional
CC CC coactivators (By similarity).
CC CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC CC alpha and a beta/ARNT subunit (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC CC translocation in response to hypoxia (By similarity).
CC CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC CC
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CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; AJ277829; CAB96628.1; -.
CC CC HSP; Q16665; IH2K.
CC CC InterPro; IPR001092; HLH basic.
CC CC InterPro; IPR001321; HypoxindFLA.
CC CC InterPro; IPR001610; PAC.
CC CC InterPro; IPR000014; PAS.
CC CC Pfam; PF00785; PAC; 1.
CC CC PRINTS; PR01080; HYPOXIAFLA.
CC CC SMART; SM00353; HLH; 1.
CC CC SMART; SM00086; PAC; 1.
CC CC SMART; SM00091; PAS; 2.
CC CC PROSITE; PS00888; HLH; 1.
CC CC PROSITE; PS0112; PAS; 2.
CC CC Activator; DNA-binding; Nuclear protein; Repeat;
CC CC Transcription regulation.
CC CC DNA BIND 17 30 Basic motif.
CC CC DOMAIN 31 71 Helix-loop-helix motif.
CC CC FT DOMAIN 85 157 PAS 1.
CC CC FT DOMAIN 229 300 PAS 2.
CC CC FT DOMAIN 303 346 PAC.
CC CC SEQUENCE 805 AA; 90964 MW; BABFA0BD6B44FF3B CRC64;

Query Match 100.0%; Score 101; DB 1; Length 805;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 552 DLDLEMLAPYIPMDDDFQL 570

RESULT 7
HIFA CHICK STANDARD; PRT; 811 AA.
AC Q9YIB9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Heart;
RA Takahashi T.;
RT Molecular cloning and expression of an avian cDNA for hypoxia-
inducible factor-1 alpha in embryonic ventricular myocytes.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a master transcriptional regulator of the

```

```

CC CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC CC [AG]CTGTG-3' within the hypoxia response element (HRE) of target
CC CC gene promoters. Activation requires recruitment of transcriptional
CC CC coactivators (By similarity).
CC CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC CC alpha and a beta/ARNT subunit (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC CC translocation in response to hypoxia (By similarity).
CC CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC CC domains, NTAD and CTAD, which function synergistically. Their
CC CC transcriptional activity is repressed by an intervening inhibitory
CC CC domain (ID) (By similarity).
CC CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC CC
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; AB013746; BAA34234.2; -.
CC CC HSP; Q16665; IH2K.
CC CC InterPro; IPR001092; HLH basic.
CC CC InterPro; IPR001321; HypoxindFLA.
CC CC InterPro; IPR001610; PAC.
CC CC InterPro; IPR000014; PAS.
CC CC Pfam; PF00785; PAC; 1.
CC CC Pfam; PF00989; PAS; 2.
CC CC PRINTS; PR01080; HYPOXIAFLA.
CC CC SMART; SM00353; HLH; 1.
CC CC SMART; SM00086; PAC; 1.
CC CC SMART; SM00091; PAS; 2.
CC CC PROSITE; PS00888; HLH; 1.
CC CC PROSITE; PS0112; PAS; 2.
CC CC Activator; DNA-binding; Nuclear protein; Repeat;
CC CC Transcription regulation.
CC CC DNA BIND 17 30 Basic motif.
CC CC DOMAIN 31 71 Helix-loop-helix motif.
CC CC FT DOMAIN 80 157 PAS 1.
CC CC FT DOMAIN 228 298 PAS 2.
CC CC FT DOMAIN 302 345 PAC.
CC CC FT DOMAIN 401 587 ODD.
CC CC FT DOMAIN 529 573 ID.
CC CC FT DOMAIN 703 706 Nuclear localization signal (Potential).
CC CC FT DOMAIN 718 721 Nuclear localization signal (Potential).
CC CC FT DOMAIN 771 811 CTAD.
CC CC FT DOMAIN 583 588 Poly-Ser.
CC CC SEQUENCE 811 AA; 90542 MW; DL4CD9FC98F064CB CRC64;

Query Match 100.0%; Score 101; DB 1; Length 811;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 554 DLDLEMLAPYIPMDDDFQL 572

RESULT 8
QYISE5
ID QYISE5 PRELIMINARY; PRT; 819 AA.
AC QYISE5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 1 alpha subunit.
OS Oryctolagus cuniculus (Rabbit).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Clausen I., Kletz S., Fischer B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY273790; AAP43517.1; -.
DR HSP; Q16665; I12K.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 819 AA; 91284 MW; E11B4FBF7D4F6C7C CRC64;

Query Match 100.0%; Score 101; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYPMDDDFQL 19
DB 556 DLDLEMLAPYPMDDDFQL 574

RESULT 9
Q64F54
ID Q64F54 PRELIMINARY; PRT; 821 AA.
AC Q64F54;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypoxia-inducible factor 1 alpha subunit.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Morin P. Jr., Storey K.B.;
RC TISSUE=Liver;
RT "Cloning and expression of HIF-1 from the hibernating ground squirrel,
RT Sperophilus tridecemlineatus."
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY173478; AAU14021.1; -.
SQ SEQUENCE 821 AA; 92028 MW; 4C96BD0355CCCE06 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 821;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYPMDDDFQL 19
DB 556 DLDLEMLAPYPMDDDFQL 574

RESULT 10
HIFA_BOVIN
ID HIFA_BOVIN STANDARD; PRT; 823 AA.
AC Q9XTA5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA Hara S., Kobayashi C., Imura N.;
RT "Molecular cloning of cDNA encoding hypoxia-inducible factor (HIF) -
RT 1alpha and -2alpha of bovine arterial endothelial cells."
RL Biochim. Biophys. Acta 1445:237-243(1999).
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBBP and
CC EP300. Activity is enhanced by interaction with both, NCOA1 or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-564 in the
CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-564.
CC The hydroxylated prolines promote interaction with VHL, initiating
CC rapid ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
CC attenuated, resulting in stabilization (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Asn-800 by HIF1AN, thus
CC abrogating interaction with CREBBP and EP300 and preventing
CC transcriptional activation (By similarity).
CC -1- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC nitrosylation in vitro, however not all thiol groups seem to be
CC nitrosylated in vivo (By similarity).
CC -1- PTM: Acetylation of Lys-532 by ARD1 increases interaction with VHL
CC and stimulates subsequent proteasomal degradation (By similarity).
CC -1- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
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CC or send an email to license@sib.ac.uk.
CC -----
CC EMBL; AB018398; BAA78675.1; -.
CC HSP; Q16665; I18C.
CC InterPro; IPR001092; HLH_basic.
CC InterPro; IPR001321; Hypoxindf1A.

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InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00010; HLH; 1.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PRO1080; HYPOMAI1A1.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS50988; HLH; 1.
PROSITE; PS50112; PAS; 2.
Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
Nuclear localization signal (Potential).
DOMAIN 718 721
FT DNA BIND 17 30
FT DOMAIN 31 71
FT DOMAIN 85 158
FT DOMAIN 228 298
FT DOMAIN 302 345
FT DOMAIN 401 600
FT DOMAIN 531 575
FT DOMAIN 576 782
FT DOMAIN 783 823
FT DOMAIN 715 718
FT MOD_RES 90 90
FT MOD_RES 139 139
FT MOD_RES 173 173
FT MOD_RES 194 194
FT MOD_RES 210 210
FT MOD_RES 219 219
FT MOD_RES 224 224
FT MOD_RES 255 255
FT MOD_RES 334 334
FT MOD_RES 337 337
FT MOD_RES 359 359
FT MOD_RES 402 402
FT MOD_RES 520 520
FT MOD_RES 532 532
FT MOD_RES 564 564
FT MOD_RES 755 755
FT MOD_RES 777 777
FT MOD_RES 797 797
FT MOD_RES 800 800
SEQUENCE 823 AA; 92127 MW; 12674E467A61B1A1 CRC64;
Query Match 100.0%; Score 101; DB 1; Length 823;
Best Local Similarity 100.0%; Pred. No. 1e-07; 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPIPMDDDFOL 19
DB 556 DLDLEMLAPIPMDDDFOL 574
PRT; 823 AA.
PRELIMINARY;
Q61V47
AC Q61V47
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia inducible factor-1a.
GN Name=HIF-1a;
OS Bos mutus grunniens (Yak).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=30521;
RN [1]
SEQUENCE FROM N.A.
RP Dolt K.S., Qadar Pasha M.A.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RC euk. similarity. Contains 1 basic helix-loop-helix (bHLH) domain.

DR PRINTS; PR01080; HYPOXIA1F1A.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS00888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 824 AA; 92161 MW; 33A1DDC3593CBFFP CRC64;
 Query Match 100.0%; Score 101; DB 2; Length 824;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 556 DLDLEMLAPYIPMDDDFQL 574
 RESULT 13
 HIFA RAT
 ID HIFA RAT
 AC O35800; Q9WTU9; STANDARD; PRT; 825 AA.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN Name=Hif1a.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Hepatocytes;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
 RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perinuclear expression of the mRNA of the three hypoxia-inducible
 factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
 RL Biochem. J. 354:531-537(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=21417706; PubMed=11526200;
 RA Zou A.-P., Yang Z.-Z., Li P.-L., Cowley A.W. Jr.;
 RT "Oxygen-dependent expression of hypoxia-inducible factor-1alpha in
 renal medullary cells of rats.";
 RL Physiol. Genomics 6:159-168(2001).
 CC -!- FUNCTION: Functions as a master transcriptional regulator of the
 adaptive response to hypoxia. Under hypoxic conditions activates
 the transcription of over 40 genes, including, erythropoietin,
 glucose transporters, glycolytic enzymes, vascular endothelial
 growth factor, and other genes whose protein products increase
 oxygen delivery or facilitate metabolic adaptation to hypoxia.
 CC Plays an essential role in embryonic vascularization, tumor
 angiogenesis and pathophysiology of ischemic disease. Binds to
 core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
 element (HRE) of target gene promoters. Activation requires
 recruitment of transcriptional coactivators such as CREBBP and
 EP300. Activity is enhanced by interaction with both, NCOAL or
 NCOA2. Interaction with redox regulatory protein APEX seems to
 activate CTAD and potentiates activation by NCOAL and CREBBP (By
 similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 alpha and a beta/ARNT subunit. Binds to the TA2-type 1 domains of
 CREBBP and EP300. Interacts with NCOAL, NCOA2, APEX and HSP90 (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
 translocation in response to hypoxia (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is
 seen in the renal medulla than in the cortex. Expressed also in
 the perivenous zone of the liver.
 CC -!- DOMAIN: Contains two independent C-terminal transactivation
 domains, NTAD and CTAD, which function synergistically. Their
 transcriptional activity is repressed by an intervening inhibitory
 domain (ID) (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the
 oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
 EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563.
 CC The hydroxylated prolines promote interaction with VHL, initiating
 rapid ubiquitination and subsequent proteasomal degradation. Under
 hypoxia, proline hydroxylation is impaired and ubiquitination is
 attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus
 abrogating interaction with CREBBP and EP300 and preventing
 transcriptional activation (By similarity).
 CC -!- PTM: S-nitrosylated. All free thiol groups are subjected to S-
 nitrosylation in vitro, however not all thiol groups seem to be
 nitrosylated in vivo (By similarity).
 CC -!- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL
 and stimulates subsequent proteasomal degradation (By similarity).
 CC -!- PTM: Phosphorylation is required for DNA binding (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; Y09507; CA070701.1; -.
 CC HSSP; AF057308; AAD24413.1; -.
 CC HSSP; Q16665; IL8C.
 CC TRANSFAC; T05461; -.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001321; Hypoxindf1A.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR01080; HYPOXIA1F1A.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC PROSITE; PS00888; HLH; 1.
 CC PROSITE; PS50112; PAS; 2.
 CC Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
 KW Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
 FT DOMAIN 718 721 Nuclear localization signal (Potential).
 FT DNA BIND 17 30 Basic motif.
 FT DOMAIN 31 71 Helix-loop-helix motif.
 FT DOMAIN 85 158 PAS 1.
 FT DOMAIN 228 298 PAS 2.
 FT DOMAIN 302 345 PAC.
 FT DOMAIN 401 602 ODD.
 FT DOMAIN 530 574 NTAD.
 FT DOMAIN 575 784 ID.
 FT DOMAIN 717 720 Nuclear localization signal (Potential).
 FT DOMAIN 785 825 CTAD.
 FT MOD_RES 90 90 S-nitrosocysteine (Potential).
 FT MOD_RES 139 139 S-nitrosocysteine (Potential).
 FT MOD_RES 173 173 S-nitrosocysteine (Potential).
 FT MOD_RES 194 194 S-nitrosocysteine (Potential).
 FT MOD_RES 210 210 S-nitrosocysteine (Potential).
 FT MOD_RES 219 219 S-nitrosocysteine (Potential).
 FT MOD_RES 224 224 S-nitrosocysteine (Potential).
 FT MOD_RES 255 255 S-nitrosocysteine (Potential).
 FT MOD_RES 334 334 S-nitrosocysteine (Potential).
 FT MOD_RES 337 337 S-nitrosocysteine (Potential).
 FT MOD_RES 385 385 S-nitrosocysteine (Potential).
 FT MOD_RES 402 402 Hydroxyproline (By similarity).
 FT MOD_RES 519 519 S-nitrosocysteine (Potential).
 FT MOD_RES 531 531 N6-acetyllysine (By similarity).

FT MOD_RES 563 Hydroxyproline (By similarity).
 FT MOD_RES 779 S-nitrosocysteine (Potential).
 FT MOD_RES 799 S-nitrosocysteine (Potential).
 FT MOD_RES 802 3-hydroxyasparagine (By similarity).
 FT CONFLICT 12 K -> NR (in Ref. 2).
 FT CONFLICT 74 D -> G (in Ref. 2).
 FT CONFLICT 96 P -> L (in Ref. 2).
 FT CONFLICT 329 D -> N (in Ref. 2).
 FT CONFLICT 613 ATATTAT -> TATA (in Ref. 2).
 FT CONFLICT 708 R -> K (in Ref. 2).
 SQ SEQUENCE 825 AA; 92319 MW; C4109A57386667E9 CRC64;
 Query Match 100.0%; Score 101; DB 1; Length 825;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYPMDDDFQL 19
 DB 555 DLDLEMLAPYPMDDDFQL 573
 RESULT 14
 HIFA_HUMAN
 ID HIFA_HUMAN STANDARD; PRT; 826 AA.
 AC Q16665; Q96P79; Q9UPB1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
 DE interacting protein) (Member of PAS protein 1) (MOP1).
 OS Homo sapiens (Human).
 GN HIF1A;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
 RX MEDLINE=95296340; PubMed=753918;
 RA Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;
 RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
 RT heterodimer regulated by cellular O2 tension.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hepatoma;
 RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
 RA Hogenesch J.B.; Chan W.K.; Jackiw V.H.; Brown R.C.; Gu Y.-Z.;
 RA Pray-Grant M.; Perdew G.H.; Bradford C.A.;
 RT "Characterization of a subset of the basic-helix-loop-helix-PAS
 RT superfamily that interacts with components of the dioxin signaling
 RT pathway.";
 RL J. Biol. Chem. 272:8581-8593(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=9900835; PubMed=9782081; DOI=10.1006/geno.1998.5416;
 RA Iyer N.V., Leung S.W., Semenza G.L.;
 RT "The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
 RT evolutionary conservation.";
 RL Genomics 52:159-165(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Rupert J.L., Hochachka P.W.;
 RT "HIF1a sequence in the Quechua, a high altitude population.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Glial tumor;
 RA Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Liver;
 RA Tanaka S., Sugimachi K.

RT "Hypoxia-inducible factor-1 alpha variant isolated from human liver
 RT tissue.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Choriocarcinoma, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP TRANSACTIVATION DOMAINS NTAD AND CTAD.
 RX MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;
 RA Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;
 RT "Transactivation and inhibitory domains of hypoxia-inducible factor
 RT 1alpha. Modulation of transcriptional activity by oxygen tension.";
 RL J. Biol. Chem. 272:19253-19260(1997).
 RN [9]
 RP SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.
 RX MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;
 RA Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,
 RA Poellinger L.;
 RT "Signal transduction in hypoxic cells: inducible nuclear translocation
 RT and recruitment of the CBP/p300 coactivator by the hypoxia-inducible
 RT factor-1alpha.";
 RL EMBO J. 17:6573-6586(1998).
 RN [10]
 RP OXYGEN-DEPENDENT DEGRADATION DOMAIN.
 RX MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;
 RA Huang L.E., Gu J., Schau M., Bunn H.F.;
 RT "Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-
 RT dependent degradation domain via the ubiquitin-proteasome pathway.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992(1998).
 RN [11]
 RP TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
 RP MUTAGENESIS OF CYS-800.
 RX MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
 RA Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
 RA Poellinger L., Fujii-Kuriyama Y.;
 RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
 RT in response to hypoxia: their stabilization and redox signal-induced
 RT interaction with CBP/p300.";
 RL EMBO J. 18:1905-1914(1999).
 RN [12]
 RP INTERACTION WITH NCOA1, NCOA2 AND APEX.
 RX MEDLINE=20063199; PubMed=10594042;
 RA Carrero P., Okamoto K., Coumalleau P., O'Brien S., Tanaka H.,
 RA Poellinger L.;
 RT "Redox-regulated recruitment of the transcriptional coactivators CREB-
 RT binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";
 RL Mol. Cell. Biol. 20:402-415(2000).
 RN [13]
 RP MUTAGENESIS OF SER-551 AND THR-552.
 RX MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;
 RA Sutter C.H., Laughner E., Semenza G.L.;
 RT "Hypoxia-inducible factor 1alpha protein expression is controlled by

RT oxygen-regulated ubiquitination that is disrupted by deletions and
RT missense mutations.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753 (2000).
RN [14]
RP UBIQUITINATION.
RX MEDLINE=21214630; PubMed=11292861; DOI=10.1126/science.1059796;
RA Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
RA Gaskell S.J., von Kriegshelm A., Hebestreit H.F., Mukherji M.,
RA Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.,
RA "Targeting of HIF-1alpha to the von Hippel-Lindau ubiquitylation
RT complex by O2-regulated prolyl hydroxylation.";
RL Science 292:468-472 (2001).
RN [15]
RP S-NITROSYLATION.
RX MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793 (02)03887-5;
RA Sumbayev V.V., Budde A., Zhou J., Bruene B.;
RT "HIF-1 alpha protein as a target for S-nitrosation.";
RL FEBS Lett. 535:106-112 (2003).
RN [16]
RP ACETYLATION OF LYS-532.
RX MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674 (02)01085-1;
RA Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
RA Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
RT "Regulation and destabilization of HIF-1alpha by ARD1-mediated
RT acetylation.";
RL Cell 111:709-720 (2002).
RN [17]
RP HYDROXYLATION OF ASN-803.
RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA Bruick R.K.;
RT "FH-1 is an asparaginyl hydroxylase enzyme that regulates the
RT transcriptional activity of hypoxia-inducible factor.";
RL Genes Dev. 16:1466-1471 (2002).
RN [18]
RP HYDROXYLATION OF PRO-402 AND PRO-564.
RX MEDLINE=21558830; PubMed=11598268; DOI=10.1126/science.1066373;
RA Bruick R.K., McKnight S.L.;
RT "A conserved family of prolyl-4-hydroxylases that modify HIF.";
RL Science 294:1337-1340 (2001).
RN [19]
RP REVIEW.
RX MEDLINE=20407247; PubMed=10950862;
RA Semenza G.L.;
RT "HIF-1 and human disease: one highly involved factor.";
RL Genes Dev. 14:1983-1991 (2000).
RN [20]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=20539371; PubMed=11089639;
RA Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
RA Michiels C.;
RT "A model for the complex between the hypoxia-inducible factor-1 (HIF-
RT 1) and its consensus DNA sequence.";
RL J. Biol. Struct. Dyn. 18:169-179 (2000).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
RP HIF1AN.
RX MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
RA Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.P.,
RA Schlemmer I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
RT "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
RT mechanism of oxidative modification of HIF-1 alpha.";
RL J. Biol. Chem. 278:1802-1806 (2003).
RN [22]
RP STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
RX MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
RA Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
RA Wagner G., Eck M.J.;
RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
RT factor-1 alpha.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372 (2002).
RN [23]
RP STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.

RX MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
RA Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
RA Wright P.E.;
RT "Structural basis for Hif-1 alpha /CBP recognition in the cellular
Query Match 100.0%; Score 101; DB 1; Length 826;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574
RESULT 15
HIFA_MOUSE
ID_HIFA_MOUSE STANDARD; PRT: 836 AA
AC Q61221; O08741; O08993; Q61664; Q61665; Q8C681; Q8CC19; Q8CCB6;
AC Q8R385; Q9CYA8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (ARNT
DE interacting protein).
GN Name=Hif1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Hepatocytes;
RX MEDLINE=96355491; PubMed=8702901; DOI=10.1074/jbc.271.35.21262;
RA Li H., Ko H.P., Whitlock J.P. Jr.;
RT "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
RT Roles of Arnt and Hif1alpha.";
RL J. Biol. Chem. 271:21262-21267 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=129/SvJ;
RX MEDLINE=98034461; PubMed=9368100;
RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
RA Bradfield C.A.;
RT "Molecular characterization of the murine Hif-1 alpha locus.";
RL Gene Expr. 6:287-299 (1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=129/SvJ;
RX MEDLINE=97354184; PubMed=9210478;
RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
RA Gassmann M.;
RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
RT organization, expression and characterization of an alternative first
RT exon and 5' flanking sequence.";
RL Eur. J. Biochem. 246:155-165 (1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Colon, Diaphragm, Embryo, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mik H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Borje A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Havaehizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast tumor;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 13-822 FROM N.A. (ISOFORM 2).
RC TISSUE=Hepatocytes;
RX MEDLINE=96254028; PubMed=8660378; DOI=10.1006/bbrc.1996.0845;
RA Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.,
RT "Nucleotide sequence, chromosomal assignment and mRNA expression of
RT mouse hypoxia-inducible factor-1 alpha.";
RL Biochem. Biophys. Res. Commun. 223:54-59 (1996).
RN [7]
RP SEQUENCE OF 22-85 FROM N.A.
RC TISSUE=Hepatocytes;
RA O'Rourke J.F.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBSJ databases.
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBBP and
CC EP300. Activity is enhanced by interaction with both, NCOA1 or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CREAD and potentiates activation by NCOA1 and CREBBP (By
CC similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q61221-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q61221-2; Sequence=VSP_007739;
CC TISSUE SPECIFICITY: Ubiquitous.
CC -1- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-577 in the
CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-577.
CC The hydroxylated prolines promote interaction with VHL, initiating
CC rapid ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
CC attenuated, resulting in stabilization on Asn-813 by HIF1A, thus
CC -1- PTM: In normoxia, is hydroxylated on Asn-813 by HIF1A, thus
CC abrogating interaction with CREBBP and EP300 and preventing
CC transcriptional activation (By similarity).
CC -1- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC nitrosylation in vitro, however not all thiol groups seem to be
CC -1- PTM: Acetylation of Lys-545 by ARD1 increases interaction with VHL
CC and stimulates subsequent proteasomal degradation (By similarity).
CC -1- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U59496; AAC52730.1; --
CC EMBL; AF003695; AAC53455.1; --
CC EMBL; Y13656; CAA70306.1; JOINED.
CC EMBL; Y13656; CAA70306.1; JOINED.
CC EMBL; Y13656; CAA70306.1; JOINED.
CC EMBL; AF004155; AAC53461.1; JOINED.
CC EMBL; AF004141; AAC53461.1; JOINED.
CC EMBL; AF004142; AAC53461.1; JOINED.
CC EMBL; AF004143; AAC53461.1; JOINED.
CC EMBL; AF004144; AAC53461.1; JOINED.
CC EMBL; AF004145; AAC53461.1; JOINED.
CC EMBL; AF004146; AAC53461.1; JOINED.
CC EMBL; AF004147; AAC53461.1; JOINED.
CC EMBL; AF004148; AAC53461.1; JOINED.
CC EMBL; AF004149; AAC53461.1; JOINED.
CC EMBL; AF004150; AAC53461.1; JOINED.
CC EMBL; AF004151; AAC53461.1; JOINED.
CC EMBL; AF004152; AAC53461.1; JOINED.
CC EMBL; AF004153; AAC53461.1; JOINED.
CC EMBL; AF004154; AAC53461.1; JOINED.
CC EMBL; AK034087; BAC28578.1; --
CC EMBL; AK076395; BAC36320.1; --
CC EMBL; AK033471; BAC28305.1; --
CC EMBL; AK017853; BAC30975.1; --
CC EMBL; BC026139; AAH26139.1; --
CC EMBL; X95580; CAA64833.1; --
CC EMBL; X95002; CAA64458.1; --
CC PIR; JC4837; JC4837.
CC TRANSFAC; T04666; --
CC MGD; MGI:106918; Hif1a.
CC GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.
CC GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.
Query Match 100.0% Score 101; DB 1; Length 836;
Best Local Similarity 100.0%; Pred. No. 1e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
 |||||
 Db 569 DLDLEMLAPYIPMDDDFQL 587

RESULT 16

ID Q9X54 PRELIMINARY; PRT; 630 AA.
 AC Q9X54;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypoxia-inducible factor 3 alpha (fragment).
 GN Name=Hif3a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
 RT "Cloning and Characterization of a Third Hypoxia Inducible Factor,
 RT HIF3-alpha.";
 RL J. Biol. Chem. 0:0-0(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99054547; PubMed=9840812;
 RA Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
 RT "Molecular characterization and chromosomal localization of a third
 RT alpha-class hypoxia inducible factor subunit, HIF3alpha.";
 RL Gene Expr. 7:205-213(1998).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AF079153; AAF21782.1; JOINED.
 DR EMBL; AF079140; AAF21782.1; JOINED.
 DR EMBL; AF079143; AAF21782.1; JOINED.
 DR EMBL; AF079145; AAF21782.1; JOINED.
 DR EMBL; AF079147; AAF21782.1; JOINED.
 DR EMBL; AF079149; AAF21782.1; JOINED.
 DR EMBL; AF079151; AAF21782.1; JOINED.
 DR EMBL; AF079152; AAF21782.1; JOINED.
 DR EMBL; AF079150; AAF21782.1; JOINED.
 DR EMBL; AF079148; AAF21782.1; JOINED.
 DR EMBL; AF079146; AAF21782.1; JOINED.
 DR EMBL; AF079144; AAF21782.1; JOINED.
 DR EMBL; AF079142; AAF21782.1; JOINED.
 DR HSSP; Q99814; IP97.
 DR MGD; MGI:1859778; Hif3a.
 DR GO; GO:0005634; C:nucleus; IC.
 DR GO; GO:0003700; F:transcription factor activity; IPI.
 DR GO; GO:0001666; P:response to hypoxia; IDA.
 DR GO; GO:0006366; P:transcription from Pol II promoter; IPI.
 DR InterPro; IPR001092; HLHbasic.
 DR InterPro; IPR001067; Nuc translocat.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS01112; PAS; 2.
 FT NON_TER 630 630
 SQ SEQUENCE 630 AA; 69623 MW; 828EB2CB4E6D45B6 CRC64;

Query Match 86.1%; Score 87; DB 2; Length 630;
 Best Local Similarity 94.4%; Pred. No. 1.6e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DLDLEMLAPYIPMDDDFQL 19

Db 480 LDLEMLAPYISMDDDFQL 497
 |||||

RESULT 17

ID Q8WXA1 PRELIMINARY; PRT; 632 AA.
 AC Q8WXA1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Inhibitory PAS domain protein.
 GN Name=IPAS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng J.Q.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AF463492; AAL69947.1; -.
 DR HSSP; Q16665; ILQ8.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLOCATR.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS01112; PAS; 2.
 SQ SEQUENCE 632 AA; 68963 MW; 9665B0AF3998F8EF CRC64;

Query Match

Best Local Similarity 86.1%; Score 87; DB 2; Length 632;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLEMLAPYIPMDDDFQL 19

Db 485 LDLEMLAPYISMDDDFQL 502
 |||||

RESULT 18

ID Q9HAI2 PRELIMINARY; PRT; 648 AA.
 AC Q9HAI2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ11591.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Whole embryo;
 RC PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,


```
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 667 AA; 72404 MW; 67B8794FF9DCCF4B CRC64;

Query Match      86.1%; Score 87; DB 2; Length 667;
Best Local Similarity 94.4%; Pred. No. 1.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLEMLAPYIPMDDDFQL 19
|||||
Db 483 LDLEMLAPYISMDDDFQL 500

RESULT 21
ID Q66K72 PRELIMINARY; PRT; 669 AA.
AC Q66K72;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE HIF3A protein.
GN Name=HIF3A;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Jones S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC080551; AAH80551.1; -
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 669 AA; 72460 MW; 7EF7362A1691AE6D CRC64;

Query Match      86.1%; Score 87; DB 2; Length 669;
Best Local Similarity 94.4%; Pred. No. 1.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLEMLAPYIPMDDDFQL 19
|||||
Db 483 LDLEMLAPYISMDDDFQL 500

RESULT 22
ID Q7T2E4 PRELIMINARY; PRT; 571 AA.
AC Q7T2E4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein hif1al.
GN Name=hif1al;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054582; AAH54582.1; -
DR HSSP; Q99814; 1P97.
DR ZFIN; ZDB-GENE-040426-1315; hif1al.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 571 AA; 63846 MW; 1BA8E4CC29F16672 CRC64;

Query Match      85.1%; Score 86; DB 2; Length 571;
Best Local Similarity 84.2%; Pred. No. 2.1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDLEMLAPYIPMDDDFQL 19
|||||
Db 430 ELDLMLAPYISMDDDFQL 448

RESULT 23
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Q6EGR9
ID Q6EGR9 PRELIMINARY; PRT; 626 AA.
AC Q6EGR9;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hif3a.
GN Name:hif3a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY330295; AAQ94179.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 626 AA; 70221 MW; EA12390DFEC9089 CRC64;

Query Match 85.1%; Score 86; DB 2; Length 626;
Best Local Similarity 84.2%; Pred. No. 2.3e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
Db 485 ELDLMLAPYISMDDDFQL 503

RESULT 24
Q6STN6
ID Q6STN6 PRELIMINARY; PRT; 643 AA.
AC Q6STN6;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypoxia-inducible factor-4alpha.
GN Name:hif-4alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY450270; AAR95698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00989; PAS; 1.

Query Match 85.1%; Score 86; DB 2; Length 626;
Best Local Similarity 84.2%; Pred. No. 2.3e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
Db 485 ELDLMLAPYISMDDDFQL 503

RESULT 24
Q6STN6
ID Q6STN6 PRELIMINARY; PRT; 643 AA.
AC Q6STN6;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypoxia-inducible factor-4alpha.
GN Name:hif-4alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY450270; AAR95698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00989; PAS; 1.

Query Match 85.1%; Score 86; DB 2; Length 643;
Best Local Similarity 84.2%; Pred. No. 2.4e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
Db 495 ELDLMLAPYISMDDDFQL 513

RESULT 25
Q9JHS2
ID Q9JHS2 PRELIMINARY; PRT; 662 AA.
AC Q9JHS2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypoxia inducible factor 3 alpha.
GN Name:hif-3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
RL Biochem. J. 354:531-537(2001).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (BHLH) domain.
DR EMBL; AJ277827; CAB96611.1; -.
DR HSP; Q99814; IP97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 662 AA; 72887 MW; AC9672E340544010 CRC64;

Query Match 82.2%; Score 83; DB 2; Length 662;
Best Local Similarity 94.1%; Pred. No. 7.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DLEMLAPYIPMDDDFQL 19
Db 481 DLEMLAPYISMDDDFQL 497

RESULT 26
Q696W2
ID Q696W2 PRELIMINARY; PRT; 835 AA.
AC Q696W2;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gernard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC074648; AAH74648.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAC; 2.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAC; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAC; 2.
DR PROSITE; PS50112; PAC; 2.
SQ SEQUENCE 862 AA; 97138 MW; C2976D62101531CE CRC64;
Query Match 79.7%; Score 80.5; DB 2; Length 862;
Best Local Similarity 85.0%; Pred. No. 0.00027;
Matches 17; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
Qy 1 DLDLEMLAPYIPMD-DDFQL 19
Db 517 DLDLETLAPYIPMDGEDFQL 536
RESULT 29
Q6GP97 PRELIMINARY; PRT; 862 AA.
AC Q6GP97;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE MGC80589 protein.
GN Name=MGC80589;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC073244; AAH73244.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAC.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAC; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAC; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAC; 2.
DR PROSITE; PS50112; PAC; 2.
SQ SEQUENCE 862 AA; 97319 MW; 3AC8FB39032E9E60 CRC64;
Query Match 79.7%; Score 80.5; DB 2; Length 862;
Best Local Similarity 85.0%; Pred. No. 0.00027;
Matches 17; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
Qy 1 DLDLEMLAPYIPMD-DDFQL 19
Db 518 DLDLETLAPYIPMDGEDFQL 537
RESULT 30
Q6QGM4 PRELIMINARY; PRT; 873 AA.
AC Q6QGM4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypoxia-inducible factor 2 alpha.
OS Fundulus heteroclitus (Killifish) (Mummichog).


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Best Local Similarity 80.0%; Pred. No. 0.00019;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAPYIPMD-DDFOL 19
:|||||:|||||:|||||
Db 118 ELDLETLAPYIPMDGEDFOL 137

RESULT 33
QRYDO PRELIMINARY; PRT; 164 AA.
AC Q6RYDO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Endothelial PAS domain protein 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Ing N.H., Balog C.J., Wolfekill R.L.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RT EMBL; AY485674; AAR37391.1; -.
FT NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 17405 MW; 49DBB95BA3D6D826 CRC64;

Query Match 75.7%; Score 76.5; DB 2; Length 164;
Best Local Similarity 80.0%; Pred. No. 0.00019;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAPYIPMD-DDFOL 19
:|||||:|||||:|||||
Db 119 ELDLETLAPYIPMDGEDFOL 138

RESULT 34
Q9W7C6 PRELIMINARY; PRT; 867 AA.
AC Q9W7C6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endothelial PAS domain protein 1.
GN Name=EPAS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=breed White Leghorn;
RC MEDLINE=20047819; PubMed=10580084; DOI=10.1016/S0014-5793(99)01476-3;
RA Favier J., Kempf H., Corvol P., Gasc J.-M.;
RT "Cloning and expression pattern of EPAS1 in the chicken embryo.
RT Colocalization with tyrosine hydroxylase.";
RL FEBS Lett. 462:19-24 (1999).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF129813; AAD38358.1; -.
DR HSSP; Q99814; 1P97.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

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DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PSS0888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 867 AA; 97133 MW; DE674A948DE11DCC CRC64;

Query Match 75.7%; Score 76.5; DB 2; Length 867;
Best Local Similarity 80.0%; Pred. No. 0.0012;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAPYIPMD-DDFOL 19
:|||||:|||||:|||||
Db 522 ELDLETLAPYIPMDGEDFOL 541

RESULT 35
PAS1_HUMAN STANDARD; PRT; 870 AA.
AC Q99814; Q86VA2; Q99630;
DT 15-DEC-1998 (Rel. 37, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Endothelial PAS domain protein 1 (EPAS1) (Member of PAS protein 2)
DE (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha)
DE (HIF-1 alpha-like factor) (HLF).
GN Name=EPAS1; Synonyms=HIF2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97152468; PubMed=9000051;
RA Tian H., McKnight S.L., Russell D.W.;
RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT selectively expressed in endothelial cells.";
RL Genes Dev. 11:72-82 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Hepatoma;
RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA Pray-Grant M., Perdev G.H., Bradfield C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS
RT superfamily that interacts with components of the dioxin signaling
RT pathway.";
RL J. Biol. Chem. 272:8581-8593 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```


RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
 RP MUTAGENESIS OF CYS-844.
 RX MEDLINE-99219869; PubMed-10202154; DOI=10.1093/emboj/18.7.1905;
 RA Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
 RA Poellinger L., Fujii-Kuriyama Y.;
 RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
 RT in response to hypoxia: their stabilization and redox signal-induced
 RT interaction with CBP/p300.";
 RT EMBO J. 18:1905-1914(1999).
 RL
 CC -!- FUNCTION: Transcription factor involved in the induction of oxygen
 CC regulated genes. Binds to core DNA sequence 5'-(AG)CGTG-3' within
 CC the hypoxia response element (HRE) of target gene promoters.
 CC Regulates the vascular endothelial growth factor (VEGF) expression
 CC and seems to be implicated in the development of blood vessels and
 CC the tubular system of lung. May also play a role in the formation
 CC of the endothelium that gives rise to the blood brain barrier.
 CC Potent activator of the Tie-2 tyrosine kinase expression.
 CC Activation seems to require recruitment of transcriptional
 CC coactivators such as CREBBP and probably EP300. Interaction with
 CC redox regulatory protein APEX seems to activate CTAD.
 CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
 CC bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
 CC in placenta, lung and heart. Selectively expressed in endothelial
 CC cells.
 CC -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-531
 CC by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
 CC prolines promote interaction with VHL, initiating rapid
 CC ubiquitination and subsequent proteasomal degradation. Under
 CC hypoxia, proline hydroxylation is impaired and ubiquitination is
 CC attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-847 by HIF1AN thus
 CC probably abrogating interaction with CREBBP and EP300 and
 CC preventing transcriptional activation (By similarity).
 CC -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U81984; ABA41495.1; -;
 CC EMBL; U51626; AAC51212.1; -;
 CC EMBL; BC051338; AAH51338.1; -;
 CC PDB; 1P97; NMR; A=237-350.
 CC TRANSFAC; T02718; -;
 CC Genew; HGNC:3374; EPAS1.
 CC MIM; 603349; -;
 CC GO; GO:0003705; F:RNA polymerase II transcription factor acti. . .; TAS.
 CC GO; GO:0003713; F:transcription coactivator activity; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC GO; GO:0006366; P:transcription from Pol II promoter; TAS.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001067; Nuc_translocat.
 CC InterPro; IPR001610; PAC.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 1.
 CC PRINTS; PR00785; NCTRNLOCATR.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS50112; PAS; 2.
 KW 3D-structure; Activator; Angiogenesis; Developmental protein;
 KW DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
 KW Transcription regulation.
 FT DNA_BIND 15 27 Basic motif.
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 436 542 NTAD.
 FT DOMAIN 830 870 CTAD.
 FT DOMAIN 474 480 Poly-Ser.
 FT MOD_RES 405 405 Hydroxyproline (By similarity).
 FT MOD_RES 531 531 Hydroxyproline (By similarity).
 FT MOD_RES 840 840 Phosphothreonine (By similarity).
 FT MOD_RES 847 847 3-hydroxyasparagine (By similarity).
 FT MUTAGEN 844 844 C->S: Abolishes hypoxia-inducible
 FT transactivation of ctad.
 FT CONFLICT 60 60 A -> E (in Ref. 1).
 FT CONFLICT 539 539 D -> G (in Ref. 2).
 FT CONFLICT 601 601 H -> R (in Ref. 2).
 FT CONFLICT 693 693 D -> N (in Ref. 2).
 FT CONFLICT 716 716 E -> K (in Ref. 2).
 FT CONFLICT 722 722 L -> P (in Ref. 2).
 FT CONFLICT 765 765 F -> L (in Ref. 2).
 FT CONFLICT 769 769 P -> S (in Ref. 2).
 FT CONFLICT 844 844 C -> R (in Ref. 2).
 FT CONFLICT 847 847 N -> K (in Ref. 2).
 SQ SEQUENCE 870 AA; 96458 MW; 4838989598234FCL CRC64;
 Query Match 75.7%; Score 76.5; DB 1; Length 870;
 Best Local Similarity 80.0%; Pred. No. 0.0013;
 Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 DLDLEMLAPYIPMD-DDFQL 19
 Db 523 ELDLETLAPYIPMDGEDFQL 542
 RESULT 36
 Q9XTA4 PRELIMINARY; PRT; 870 AA.
 AC Q9XTA4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Endothelial PAS domain protein 1/hypoxia-inducible factor-2
 DE alpha.
 GN Name=EPAS1/HIF2 alpha;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Arterial;
 RX MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
 RA Hara S., Kobayashi C., Imura N.;
 RT "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF) -
 RT 1alpha and -2alpha of bovine arterial endothelial cells.";
 RL Biochim. Biophys. Acta 1445:237-243(1999).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; AB018399; BAA78676.1; -;
 DR HSSP; Q99814; 1P97.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001092; HLH_basic.

DR InterPro; IPR001067; Nuc translocat.

DR InterPro; IPR001610; PAC-

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR00785; NCTNSLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS00888; HLH; 1.

DR PROSITE; PS0112; PAS; 2.

SQ SEQUENCE 870 AA; 96168 MW; FEC602E6012D7712 CRC64;

Query Match

Best Local Similarity 75.7%; Score 76.5; DB 2; Length 870;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAPYIPMD-DDFQL 19

:|||||:|||||:|||||

Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 37

Q9PTB3

ID Q9PTB3 PRELIMINARY; PRT; 870 AA.

AC Q9PTB3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 26, Last annotation update)

DE Hypoxia-inducible factor 2 alpha.

OS Coturnix coturnix (Common quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Coturnix.

OX NCBI_TaxID=9091;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99425185; PubMed=10495286; DOI=10.1016/S0925-4773(99)00144-6;

RA Elvert G., Lanz S., Kappel A., Flamme I.,

RT "mRNA cloning and expression studies of the quail homolog of HIF-2

alpha.";

RL Mech. Dev. 87:193-197(1999).

CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AF212989; AAF21052.1; -.

DR HSSP; Q99814; 1P97.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR001092; HLH basic.

DR InterPro; IPR001067; Nuc translocat.

DR InterPro; IPR001610; PAC.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR00785; NCTNSLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS00888; HLH; 1.

DR PROSITE; PS0112; PAS; 2.

SQ SEQUENCE 870 AA; 97803 MW; 086AC8CF1639D77C CRC64;

Query Match

Best Local Similarity 75.7%; Score 76.5; DB 2; Length 870;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAPYIPMD-DDFQL 19

:|||||:|||||:|||||

Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 38

PAS1 MOUSE

ID PAS1 MOUSE STANDARD; PRT; 874 AA.

AC P97481; O08787; O50046;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2

alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (MHLF)

DE (HIF-related factor) (HRF).

GN Name=Epas1; Synonym=Hif2a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97152468; PubMed=9000051;

RA Tian H., McKnight S.L., Russell D.W.;

RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor

selectively expressed in endothelial cells.";

RL Genes Dev. 11:72-82(1997).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Hypothalamus, and Skeletal muscle;

RX MEDLINE=97272213; PubMed=9113979; DOI=10.1073/pnas.94.9.4273;

RA Ema M., Taya S., Yokotani N., Sogawa K., Matsuda Y.,

RA Fujii-Kuriyama Y.;

RT "A novel bHLH-PAS factor with close sequence similarity to hypoxia-

inducible factor alpha regulates the VEGF expression and is

potentially involved in lung and vascular development.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain capillary;

RX MEDLINE=97321546; PubMed=9178256; DOI=10.1016/S0925-4773(97)00674-6;

RA Flamme I., Froehlich I., von Reutern M., Kappel A., Damert A.,

RA Risau W.;

RT "HRF, a putative basic helix-loop-helix-PAS-domain transcription

factor is closely related to hypoxia-inducible factor-1 alpha and

developmentally expressed in blood vessels.";

RL Mech. Dev. 63:51-60(1997).

[4]

RP SEQUENCE OF 846-864, AND MUTAGENESIS OF PRO-530 AND ASN-851.

RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;

RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,

RA Bruick R.K.;

RT "HIF-1 is an asparaginyl hydroxylase enzyme that regulates the

transcriptional activity of hypoxia-inducible factor.";

RL Genes Dev. 16:1466-1471(2002).

[5]

RP INTERACTION WITH CREBBP, PHOSPHORYLATION SITE THR-844, AND MUTAGENESIS

OF THR-844.

RX MEDLINE=22075202; PubMed=11983697; DOI=10.1074/jbc.M201307200;

RA Gradin K., Takasaki C., Fujii-Kuriyama Y., Sogawa K.;

RT "The transcriptional activation function of the HIF-like factor

requires phosphorylation at a conserved threonine.";

RL J. Biol. Chem. 277:23508-23514(2002).

[6]

RP HYDROXYLATION OF ASN-851.

RX MEDLINE=21682001; PubMed=11823643; DOI=10.1126/science.1068592;

RA Lando D., Peet D.J., Whelan D.A., Gorman J.J., Whitelaw M.L.;

RT "Asparagine hydroxylation of the HIF transcription domain a hypoxic

switch.";

RL Science 295:858-861(2002).

-!- FUNCTION: Transcription factor involved in the induction of oxygen

regulated genes. Binds to core DNA sequence 5'-(AG)CGTG-3' within

the hypoxia response element (HRE) of target gene promoters.

CC Regulates the vascular endothelial growth factor (VEGF) expression

and seems to be implicated in the development of blood vessels and

the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier.
 Potent activator of the Tie-2 tyrosine kinase expression.
 Activation requires recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).
 -!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP.
 -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels in lung, followed by heart, kidney, brain and liver. Predominantly expressed in endothelial cells. Also found in smooth muscle cells of the uterus, neurons, and brown adipose tissue. High expression in embryonic choroid plexus and kidney glomeruli.
 -!- DEVELOPMENTAL STAGE: In day 11 embryo, expression is almost exclusively seen in endothelial cells of the intersegmental blood vessels separating the somites, the atrial and ventricular chambers of the heart, and the dorsal aorta. High expression also occurs in extra-embryonic membranes. In the developing brain of day 13 embryo, endothelial cells of the highly vascularized choroid plexus contain high levels of EPAS1.
 -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530 by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).
 -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus probably abrogating interaction with CREBBP and EP300 and preventing transcriptional activation.
 -!- PTM: Phosphorylated on multiple sites in the CTAD.
 -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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 EMBL; U01983; AAB41496.1; -
 EMBL; D89787; BAA20130.1; -
 EMBL; AF045160; AAC12871.1; -
 HSP; Q16665; 1H2K.
 TRANSFAC; T02719; -
 MGD; MGI:109169; Epas1.
 InterPro; IPR001092; HLH basic.
 InterPro; IPR001067; Nuc translocat.
 InterPro; IPR001610; PAC.
 InterPro; IPR000014; PAS.
 Pfam; PF00010; HLH; 1.
 Pfam; PF00785; PAC; 1.
 Pfam; PF00989; PAS; 1.
 PRINTS; PR00785; NCTRNLOCATR.
 SMART; SM00353; HLH; 1.
 SMART; SM00086; PAC; 1.
 SMART; SM00091; PAS; 2.
 TIGRFAMs; TIGR00229; sensory_box; 2.
 PROSITE; PS50888; HLH; FALSE_NEG.
 PROSITE; PS50112; PAS; 2.
 KW Activator; Angiogenesis; Developmental protein;
 Direct protein sequencing; DNA-binding; Hydroxylation;
 Nuclear protein; Phosphorylation; Repeat; Transcription regulation.
 FT DNA BIND 15 27
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT PAS 1.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 NTAD.
 FT DOMAIN 834 874 CTAD.

Poly-Ser.
 Hydroxyproline (By similarity).
 Hydroxyproline (By similarity).
 Phosphothreonine.
 3-hydroxyasparagine.
 P->A: Confers transcriptional activity at normoxia; when associated with CREBBP.
 T->A: Decreases interaction with CREBBP.
 N->A: Confers transcriptional activity at normoxia; when associated with A-530.
 C->S (in Ref. 2).
 K->KS (in Ref. 1).
 VS->AA (in Ref. 3).
 D->G (in Ref. 3).
 G->V (in Ref. 2).
 A->P (in Ref. 2).
 S->W (in Ref. 1).
 P->L (in Ref. 1).
 P->E (in Ref. 1).
 D->E (in Ref. 3).
 P->L (in Ref. 3).
 A->G (in Ref. 3).
 P->L (in Ref. 3).
 S->F (in Ref. 3).
 S->N (in Ref. 3).
 SQ SEQUENCE 874 AA; 96712 MW; A6FFA490AE43640C CRC64;
 Query Match 75.7%; Score 76.5; DB 1; Length 874;
 Best Local Similarity 80.0%; Pred. No. 0.0013;
 Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 DIDLEMLAPYPMDDDFQL 19
 :|||||:|||||:|||||
 DB 522 ELDLETLAPYPMDDGFQL 541
 RESULT 39
 PAS1_RAT STANDARD; PRT; 874 AA.
 AC Q9JHS1.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha).
 GN Name=Epas1; Synonyms=Hif2a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
 RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perivenous expression of the mRNA of the three hypoxia-inducible factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
 RL Biochem. J. 354:531-537(2001).
 CC -!- FUNCTION: Transcription factor involved in the induction of oxygen regulated genes. Binds to core DNA sequence 5'-[AG]CTG-3' within the hypoxia response element (HRE) of target gene promoters. Regulates the vascular endothelial growth factor (VEGF) expression and seems to be implicated in the development of blood vessels and the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier.
 CC Potent activator of the Tie-2 tyrosine kinase expression.
 CC Activation seems to require recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -!- PTM: In normoxia, is probably hydroxylated on pro-405 and pro-530
 CC by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
 CC prolines promote interaction with VHL, initiating rapid
 CC ubiquitination and subsequent proteasomal degradation. Under
 CC hypoxia, proline hydroxylation is impaired and ubiquitination is
 CC attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus
 CC probably abrogating interaction with CREBBP and EP300 and
 CC preventing transcriptional activation (By similarity).
 CC -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ277828; CAB96612.1; -;
 CC HSP; Q16665; 1H2K.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001067; Nuc_translocat.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR00785; NCTRNSLOCATR.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 1.
 CC TIGRFAMs; TIGR00229; sensory_box; 2.
 CC PROSITE; PS00888; HLH; FALSE_NEG.
 CC PROSITE; PS0112; PAS; 2.
 CC KW Activator; Angiogenesis; Developmental protein; DNA-binding;
 KW Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
 KW Transcription regulation.
 FT DNA_BIND 15 27
 FT DOMAIN 28 68 Basic motif.
 FT DOMAIN 84 154 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 NTAD.
 FT DOMAIN 834 874 CTAD.
 FT DOMAIN 474 479 Poly-Ser.
 FT MOD_RES 405 405 Hydroxyproline (By similarity).
 FT MOD_RES 530 530 Hydroxyproline (By similarity).
 FT MOD_RES 844 844 Phosphothreonine (By similarity).
 FT MOD_RES 851 851 3-hydroxyasparagine (By similarity).
 SQ SEQUENCE 874 AA; 96718 MW; 1A1F08EBE24369796 CRC64;

Query Match 75.7%; Score 76.5; DB 1; Length 874;
 Best Local Similarity 80.0%; Pred. No. 0.0013;
 Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 DLDLEMLAPYIPMD-DDFQL 19
 :|||||:|||||:|||||
 Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 40
 Q6PEU2 PRELIMINARY; PRT; 874 AA.
 AC Q6PEU2
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Endothelial PAS domain protein 1.
 GN Name=Epas1;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC EMBL; BC057870; AAH57870.1; -;
 CC GO; GO:0005634; C:nucleus; IEA.
 CC GO; GO:0004871; F:signal transducer activity; IEA.
 CC GO; GO:0003700; F:transcription factor activity; IEA.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 CC GO; GO:0007155; P:signal transduction; IEA.
 CC InterPro; IPR001092; HLH_basic.
 CC InterPro; IPR001067; Nuc_translocat.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 1.
 CC PRINTS; PR00785; NCTRNSLOCATR.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 874 AA; 96636 MW; 2E6D7603A678EACE CRC64;

Query Match 75.7%; Score 76.5; DB 2; Length 874;
 Best Local Similarity 80.0%; Pred. No. 0.0013;
 Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 DLDLEMLAPYIPMD-DDFQL 19
 :|||||:|||||:|||||
 Db 522 ELDLETLAPYIPMDGEDFQL 541

RESULT 41
 Q8QG15 PRELIMINARY; PRT; 235 AA.
 AC Q8QG15
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypoxia-inducible factor alpha-like protein (fragment).
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 ON NCBI_TaxID=8078;
 RX SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
 RA Powell W.H., Hahn M.E.;
 RA "Identification and functional characterization of hypoxia-inducible
 RT factor 2alpha from the estuarine teleost, Fundulus heteroclitus;
 RT interaction of HIF-2alpha with two ARNT2 splice variants.";
 RL J. Exp. Zool. 294:17-29(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Oleksak M.P., Kellell K.J., Crawford D.L., Hahn M.E., Powell W.H.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF433668; AM12473.1; -;
 DR HSP; Q99814; I997.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001610; PAC.
 DR SMART; SM00086; PAC; 1.
 FT NON_TER 1
 FT NON_TER 235
 SQ SEQUENCE 235 AA; 25400 MW; AE7A7C5D15827351 CRC64;
 Query Match 64.4%; Score 65; DB 2; Length 235;
 Best Local Similarity 80.0%; Pred. No. 0.023;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DLEMLAPYIPMDDDF 17
 DB 221 ELEMVAPYISMDDDF 235
 RESULT 42
 SIMA DROME
 ID SIMA DROME STANDARD; PRT; 1507 AA.
 AC Q24167; Q9VAAS;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Similar protein.
 GN Name=sima; ORFNames=CG7951;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=96269413; PubMed=8682312; DOI=10.1016/0378-1119(96)00060-1;
 RA Nambo J.R., Chen W., Hu S., Crews S.T.;
 RA "The Drosophila melanogaster similar bHLH-PAS gene encodes a protein
 RT related to human hypoxia-inducible factor 1 alpha and Drosophila
 RT single-minded.";
 RL Gene 172:249-254 (1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin M., Houston K.A., Howland T.J., Wei M.-H., Ibegwag K.A.,
 Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Mohrefi A.,
 Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 Palazzolo M., Pittman G.S., Pan S., Plessker D.R., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RN [3]
 RN GENOME REANNOTATION.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 Bettencourt B.R., Celinker S.E., de Grey A.D.N.-J., Drysdale R.A.,
 Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Lewis S.E.;
 RA "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -!- FUNCTION: Possible DNA-binding transcriptional activator.
 CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
 CC bHLH protein.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed in the embryo.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
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 CC -----
 DR EMBL; U43090; AAC47303.1; -;
 DR EMBL; AE003772; AAF57008.2; -;
 DR FIR; JC4851; JC4851.
 DR FlyBase; FBgn0015542; sima.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00785; PAC; 1.
 DR Pfam; PF00989; PAS; 1.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS50888; HLH; FALSE_NEG.
 DR PROSITE; PS50112; PAS; 2.
 KW Activator; Coiled coil; DNA-binding; Nuclear protein; Repeat;

Transcription regulation.

FT DNA BIND 72 85
 FT DOMAIN 86 126
 FT DOMAIN 167 240
 FT DOMAIN 307 377
 FT DOMAIN 381 422
 FT DOMAIN 577 597
 FT DOMAIN 880 908
 FT DOMAIN 982 1054
 FT DOMAIN 1110 1162
 FT DOMAIN 126 39
 FT DOMAIN 718 725
 FT DOMAIN 759 763
 FT DOMAIN 767 776
 FT DOMAIN 907 918
 FT DOMAIN 945 948
 FT DOMAIN 990 998
 FT DOMAIN 1020 1038
 FT DOMAIN 1113 1126
 FT DOMAIN 1146 1162
 FT DOMAIN 1205 1208
 FT DOMAIN 1277 1284
 FT DOMAIN 1298 1301
 FT CONFLICT 38 38
 FT CONFLICT 345 345
 FT CONFLICT 492 492
 FT CONFLICT 588 588
 FT CONFLICT 709 709
 FT CONFLICT 776 776
 FT CONFLICT 895 895
 FT CONFLICT 902 902
 FT CONFLICT 982 982
 FT CONFLICT 1125 1126
 FT CONFLICT 1154 1157
 FT CONFLICT 1444 1444
 FT CONFLICT 1447 1447
 FT CONFLICT 1451 1451
 FT CONFLICT 1494 1494
 FT CONFLICT 1507 1507
 SQ SEQUENCE 1507 AA; 165824 MW; 4102933C8FBFB0C6 CRC64;

Query Match 53.5%; Score 54; DB 1; Length 1507;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MLAPYIPWDDDFQ 19
 Db 847 MRAPYIPDDDDQ 860

RESULT 43

Qy Q8L9F9 PRELIMINARY; PRT; 293 AA.
 AC Q8L9F9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,

Basic motif.
 Helix-loop-helix motif (By similarity).
 PAS 1.
 PAS 2.
 PAS 3.
 Pro-rich.
 Coiled coil (Potential).
 Coiled coil (Potential).
 Coiled coil (Potential).
 Poly-Ser.
 Poly-Ser.
 Poly-Gln.
 Poly-Gln.
 Poly-Gln.
 Poly-Gln.
 Poly-Gln.
 Poly-Gln.
 Poly-Gln.
 Poly-Gln.
 Poly-Asp.
 S -> A (in Ref. 1).
 S -> L (in Ref. 1).
 A -> V (in Ref. 1).
 T -> I (in Ref. 1).
 T -> K (in Ref. 1).
 Q -> QQQ (in Ref. 1).
 Q -> QQ (in Ref. 1).
 G -> S (in Ref. 1).
 A -> T (in Ref. 1).
 Missing (in Ref. 1).
 Missing (in Ref. 1).
 F -> L (in Ref. 1).
 G -> C (in Ref. 1).
 S -> N (in Ref. 1).
 D -> G (in Ref. 1).

Feldmann K.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY088458; AM65994.1; -;
 DR InterPro; IPR000886; ER_target_S.
 DR InterPro; IPR005606; Sec20.
 DR Pfam; PF03908; Sec20; 1.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 293 AA; 32851 MW; 3597C4A271A31E42 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 293;
 Best Local Similarity 50.0%; Pred. No. 28;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DLEMLAPYIPWDDDFQ 18
 Db 67 NLDLAPQLPSDDQVQ 82

RESULT 44

Q8GWA6 PRELIMINARY; PRT; 293 AA.
 AC Q8GWA6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK118973; BAC43550.1; -;
 DR InterPro; IPR000886; ER_target_S.
 DR InterPro; IPR005606; Sec20.
 DR Pfam; PF03908; Sec20; 1.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 293 AA; 32818 MW; 39B8BF2001A302B0 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 293;
 Best Local Similarity 50.0%; Pred. No. 28;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DLEMLAPYIPWDDDFQ 18
 Db 67 NLDLAPQLPSDDQVQ 82

RESULT 45

Q9LK13 PRELIMINARY; PRT; 330 AA.
 AC Q9LK13;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K7M2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.

```

RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RL TAC and BAC clones.;
RN DNA Res. 7:217-221(2000).
RP SEQUENCE FROM N.A.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000382; BAB02931.1; -.
DR InterPro; IPR000886; ER target_S.
DR Pfam; PF03908; Sec20; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
SQ SEQUENCE 330 AA; 37213 MW; 9432B6B4A206A479 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 330;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 DLEMLAPYIPMDDDFQ 18
DB 104 NLDLAPQLPSPDDQVQ 119

RESULT 46
Q9AGM7 PRELIMINARY; PRT; 494 AA.
AC Q9AGM7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type II protein secretion ATPase LspE.
GN Name=lspe;
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=130B;
RX MEDLINE=21153567; PubMed=11254562;
RX DOI=10.1128/IAI.69.4.2092-2098.2001;
RA Rosier O., Cianciotto N.P.;
RT "Type II protein secretion is a subset of the Pili-dependent processes
RT that facilitate intracellular infection by Legionella pneumophila.";
RL Infect. Immun. 69:2092-2098(2001).
DR EMBL; AF330136; AAK35046.1; -.
DR HSP; P37093; 1P9R.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001482; GSPII_E.
DR Pfam; PF00437; GSPII_E; 1.
DR ProDom; PD000739; GSPII_E; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00662; T2SP_E; 1.
DR ATP-binding.
SQ SEQUENCE 494 AA; 55138 MW; E81B27C741036B0C CRC64;

Query Match 46.5%; Score 47; DB 2; Length 494;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDD 16
DB 88 DMDSMLASQLPVSDD 103

RESULT 47
Q935T8 PRELIMINARY; PRT; 562 AA.
AC Q935T8;

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transfer protein.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CNRZ368;
RX MEDLINE=95379495; PubMed=7651138;
RX Guedon G., Bourgoin F., Pebay M., Roussel Y., Colmin C., Simonet J.M.,
RA Decaris B.;
RT "Characterization and distribution of two insertion sequences, IS1191
RT and iso-IS981, in Streptococcus thermophilus: does intergeneric
RT transfer of insertion sequences occur in lactic acid bacteria co-
RT cultures?";
RL Mol. Microbiol. 16:69-78(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CNRZ368;
RX MEDLINE=20208895; PubMed=10742276;
RX DOI=10.1128/AEM.66.4.1749-1753.2000;
RX Burrus V., Roussel Y., Decaris B., Guedon G.;
RA "Characterization of a novel integrative element, ICEst1, in the
RT lactic acid bacterium Streptococcus thermophilus.";
RN [3]
RP Appl. Environ. Microbiol. 66:1749-1753(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CNRZ368;
RX MEDLINE=21178499; PubMed=11282600;
RX DOI=10.1128/AEM.67.4.1522-1528.2001;
RX Burrus V., Bontemps C., Decaris B., Guedon G.;
RA "Characterization of a novel type II restriction-modification system,
RT St3681, encoded by the integrative element ICEst1 of Streptococcus
RT thermophilus CNRZ368.";
RL Appl. Environ. Microbiol. 67:1522-1528(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CNRZ368;
RX MEDLINE=97286550; PubMed=9141697;
RX Roussel Y., Bourgoin F., Guedon G., Pebay M., Decaris B.;
RA "Analysis of the genetic polymorphism between three Streptococcus
RT thermophilus strains by comparing their physical and genetic
RT organization.";
RL Microbiology 143:1335-1343(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=CNRZ368;
RX MEDLINE=22272761; PubMed=12383726; DOI=10.1016/S0147-619X(02)00102-6;
RX Burrus V., Pavlovic G., Decaris B., Guedon G.;
RA "The ICEst1 element of Streptococcus thermophilus belongs to a large
RT family of integrative and conjugative elements that exchange module
RT and change their specificity of integration.";
RL Plasmid 48:77-97(2002).
DR EMBL; AJ278471; CAC67541.1; -.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
DR PROSITE; PS50901; FTSK; 1.
SQ SEQUENCE 562 AA; 64960 MW; 3042BFE8CEA7D84 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 562;
Best Local Similarity 47.1%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDF 17
DB 416 DLAGEFPSPYVPLDQGF 432

RESULT 48
Q70CAB

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ID Q70CAB PRELIMINARY; PRT; 562 AA.
AC Q70CAB;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transfer protein.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CNR2385;
RA Pavlovic G., Burrus V., Gintz B., Decaris B., Guedon G.;
RT "Evolution of genomic islands by deletion and tandem accretion by
RT site-specific recombination: ICEstI-related elements from
RT Streptococcus thermophilus.";
RL Microbiology 50:759-774(2004).
DR EMBL; AJ586568; CAES2361.1; -.
DR InterPro; IPR002543; FtsK SpoIIIE.
DR Pfam; PF01580; FtsK SpoIIIE; 1.
DR PROSITE; PS03001; FTSK; 1.
SQ SEQUENCE 562 AA; 65116 MW; A8A817063326D21B CRC64;

Query Match 46.5%; Score 47; DB 2; Length 562;
Best Local Similarity 47.1%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDP 17
Db 416 DLAGEFFSPYVPLDQGF 432

RESULT 49
O85306 PRELIMINARY; PRT; 113 AA.
ID O85306;
AC O85306;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PipC.
GN Name=pipC;
OS Salmonella dublin.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=98360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2229;
RA Wood M.W., Jones M.A., Watson P.R., Hedges S., Wallis T.S.,
RA Galyov E.E.;
RT "Identification of a pathogenicity island required for Salmonella
RT enteropathogenicity.";
RL Mol. Microbiol. 29:883-891(1998).
DR EMBL; AF060858; AAC33724.1; -.
DR HSPF; O30917; IK3S.
SQ SEQUENCE 113 AA; 12677 MW; 2E2BF7E0CC541709 CRC64;

Query Match 45.5%; Score 46; DB 2; Length 113;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDD 16
Db 37 DHTLEMCCPFMPLPDD 52

RESULT 50
O30917 PRELIMINARY; PRT; 113 AA.
ID O30917;
AC O30917; O7CQ87;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

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DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Invasion gene E protein (Pathogenicity island encoded protein:
DE SPI5).
GN Name=sigE; Synonyms=pipC; OrderedLocusNames=STM1090;
OS Salmonella typhimurium
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC14028s;
RX MEDLINE=98196723; PubMed=9537377;
RA Hong K.H., Miller V.L.;
RT "Identification of a novel Salmonella invasion locus homologous to
RT Shigella ipgDE.";
RL J. Bacteriol. 180:1793-1802(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AF021817; AAC46235.1; -.
DR EMBL; AE008747; AAL20022.1; -.
DR PDB; 1K3S; X-ray; A/B=1-113.
DR HSPF; O30917; IK3S.
KW Complete proteome.
SQ SEQUENCE 113 AA; 12751 MW; 34DEE3AB3944560E CRC64;

Query Match 45.5%; Score 46; DB 2; Length 113;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDD 16
Db 37 DHTLEMCCPFMPLPDD 52

Search completed: February 9, 2005, 06:00:12
Job time : 53.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 19.6667 Seconds
(without alignments)
72.119 Million cell updates/sec

Title: US-10-032-361-5
Perfect score: 101
Sequence: 1 DLDLEMLAPYIPMDDDFQL 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 65 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	19	4	US-09-959-873B-8
2	101	100.0	34	4	US-09-959-873B-9
3	101	100.0	54	4	US-09-438-833-13
4	101	100.0	116	4	US-09-438-833-8
5	101	100.0	288	4	US-09-438-833-9
6	101	100.0	301	4	US-09-438-833-10
7	101	100.0	311	4	US-09-438-833-7
8	101	100.0	532	4	US-09-949-016-7389
9	101	100.0	613	4	US-09-438-833-6
10	101	100.0	652	4	US-09-438-833-5
11	101	100.0	756	4	US-09-438-833-11
12	101	100.0	805	2	US-08-480-473B-4
13	101	100.0	805	3	US-08-915-213-4
14	101	100.0	805	3	US-09-235-217-4
15	101	100.0	805	5	PCT-US96-10251-4
16	101	100.0	810	1	US-08-785-241-7
17	101	100.0	813	4	US-09-438-833-12
18	101	100.0	826	1	US-08-785-241-6
19	101	100.0	826	2	US-08-480-473B-2
20	101	100.0	826	3	US-08-915-213-2
21	101	100.0	826	3	US-09-148-547-2
22	101	100.0	826	3	US-09-235-217-2
23	101	100.0	826	3	US-09-380-662-23
24	101	100.0	826	4	US-09-438-833-1
25	101	100.0	826	4	US-09-702-705-330
26	101	100.0	826	4	US-09-736-457-330
27	101	100.0	826	4	US-09-383-581-2

28	101	100.0	826	4	US-09-614-124B-330	Sequence 330, App
29	101	100.0	826	4	US-09-671-325-330	Sequence 330, App
30	101	100.0	826	4	US-09-589-184-330	Sequence 330, App
31	101	100.0	826	4	US-09-658-824-330	Sequence 330, App
32	101	100.0	826	4	US-09-959-873B-18	Sequence 18, Appl
33	101	100.0	826	4	US-09-949-016-6089	Sequence 6089, Ap
34	101	100.0	826	4	US-09-967-388-4	Sequence 4, Appli
35	101	100.0	826	5	PCT-US96-10251-2	Sequence 2, Appli
36	101	100.0	827	4	US-09-919-039-149	Sequence 149, App
37	89	88.1	19	4	US-09-972-784-5	Sequence 5, Appli
38	76.5	75.7	205	3	US-09-374-454-2	Sequence 2, Appli
39	76.5	75.7	870	1	US-08-785-241-4	Sequence 4, Appli
40	76.5	75.7	870	3	US-09-374-454-6	Sequence 6, Appli
41	76.5	75.7	875	1	US-08-785-241-5	Sequence 5, Appli
42	54	53.5	143	4	US-09-270-767-42631	Sequence 42631, A
43	54	53.5	1507	4	US-09-914-259-37	Sequence 37, Appl
44	45	44.6	182	4	US-09-248-796A-20521	Sequence 20521, A
45	44	43.6	8	4	US-09-959-873B-1	Sequence 1, Appli
46	44	43.6	98	4	US-09-543-681A-8077	Sequence 8077, Ap
47	43	42.6	133	4	US-09-248-796A-15417	Sequence 15417, A
48	43	42.6	820	4	US-09-489-039A-10142	Sequence 10142, A
49	42	41.6	8	4	US-09-959-873B-5	Sequence 5, Appli
50	42	41.6	650	4	US-09-583-110-3221	Sequence 3221, Ap
51	42	41.6	650	4	US-09-107-433-3515	Sequence 3515, Ap
52	42	41.6	873	4	US-09-710-279-3036	Sequence 3036, Ap
53	41.5	41.1	264	3	US-08-894-731-4	Sequence 3600, Ap
54	41.5	41.1	122	4	US-09-134-000C-3932	Sequence 4, Appli
55	41	40.6	122	4	US-09-134-000C-3932	Sequence 3932, A
56	41	40.6	411	4	US-09-248-796A-20681	Sequence 20681, A
57	41	40.6	876	1	US-08-785-071A-2	Sequence 2, Appli
58	41	40.6	876	3	US-09-012-872-2	Sequence 2, Appli
59	41	40.6	895	4	US-09-489-039A-12499	Sequence 12499, A
60	41	40.6	945	4	US-09-543-681A-4200	Sequence 4200, Ap
61	41	40.6	1498	4	US-09-252-991A-31234	Sequence 31234, A
62	40	39.6	8	4	US-09-959-873B-4	Sequence 4, Appli
63	40	39.6	201	4	US-09-489-039A-7210	Sequence 7210, Ap
64	40	39.6	251	4	US-09-107-532A-4651	Sequence 4651, Ap
65	40	39.6	306	4	US-09-270-767-46815	Sequence 46815, A

ALIGNMENTS

RESULT 1
US-09-959-873B-8
; Sequence 8, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-09-959-873B-8

Query Match 100.0%; Score 101; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9e-10;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2
US-09-959-873B-9
; Sequence 9, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-09-959-873B-9

Query Match 100.0%; Score 101; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 3
US-09-438-833-13
; Sequence 13, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; US-09-438-833-13

Query Match 100.0%; Score 101; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 26 DLDLEMLAPYIPMDDDFQL 44

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-09-438-833-8
; Sequence 8, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; US-09-438-833-8

Query Match 100.0%; Score 101; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 5
US-09-438-833-9
; Sequence 9, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; US-09-438-833-9

Query Match 100.0%; Score 101; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 6
US-09-438-833-10
; Sequence 10, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 10
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-826 of human HIF-1 alpha
US-09-438-833-10

Query Match 100.0%; Score 101; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 7
US-09-438-833-7
; Sequence 7, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 331-641 of human HIF-1 alpha
US-09-438-833-7

Query Match 100.0%; Score 101; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 226 DLDLEMLAPYIPMDDDFQL 244

RESULT 8
US-09-949-016-7389
; Sequence 7389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7389
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7389

Query Match 100.0%; Score 101; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 262 DLDLEMLAPYIPMDDDFQL 280

RESULT 9
US-09-438-833-6
; Sequence 6, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-438-833-6

Query Match 100.0%; Score 101; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 343 DLDLEMLAPYIPMDDDFQL 361

RESULT 10
US-09-438-833-5
; Sequence 5, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-652 of human HIF-1 alpha
US-09-438-833-5

Query Match 100.0%; Score 101; DB 4; Length 652;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 11
US-09-438-833-11
; Sequence 11, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants

FILE REFERENCE: 1848
CURRENT APPLICATION NUMBER: US/09/438,833
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 11
LENGTH: 756
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Subdomain
OTHER INFORMATION: 71-826 of human Hir-1 alpha
US-09-438-833-11

Query Match 100.0%; Score 101; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 486 DLDLEMLAPYIPMDDDFQL 504

RESULT 12

US-08-480-473B-4
Sequence 4, Application US/08480473B
Patent No. 5882914
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,473B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 100.0%; Score 101; DB 2; Length 805;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 535 DLDLEMLAPYIPMDDDFQL 553

RESULT 13

US-08-915-213-4
Sequence 4, Application US/08915213
Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-915-213-4

Query Match 100.0%; Score 101; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
Db 535 DLDLEMLAPYIPMDDDFQL 553

RESULT 14

US-09-235-217-4
Sequence 4, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,217

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-217-4

Query Match 100.0%; Score 101; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFOL 19
DB 535 DLDLEMLAPYIPMDDDFOL 553

RESULT 15
PCT-US96-10251-4
; Sequence 4, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10251-4

Query Match 100.0%; Score 101; DB 5; Length 805;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-217-4

Query Match 100.0%; Score 101; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFOL 19
DB 535 DLDLEMLAPYIPMDDDFOL 553

RESULT 16
US-08-785-241-7
; Sequence 7, Application US/08785241
; Patent No. 5695963
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.
; APPLICANT: Tian, Rui
; TITLE OF INVENTION: Endothelial PAS Domain Protein
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,241
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UTSD:1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-241-7

Query Match 100.0%; Score 101; DB 1; Length 810;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFOL 19
DB 543 DLDLEMLAPYIPMDDDFOL 561

RESULT 17
US-09-438-833-12
; Sequence 12, Application US/09438833
; Patent No. 6436854
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 813
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Subdomain
OTHER INFORMATION: 1-813 of human HIF-1 alpha
US-09-438-833-12

Query Match 100.0%; Score 101; DB 4; Length 813;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 18

US-08-785-241-6
Sequence 6, Application US/08785241
Patent No. 5695963
GENERAL INFORMATION:
APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
TITLE OF INVENTION: Endothelial PAS Domain Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785.241
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-785-241-6

Query Match 100.0%; Score 101; DB 1; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 19

US-08-480-473B-2
Sequence 2, Application US/08480473B
Patent No. 5882914
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480.473B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-480-473B-2

Query Match 100.0%; Score 101; DB 2; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 20

US-08-915-213-2
Sequence 2, Application US/08915213
Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 826 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-915-213-2
;
; Query Match      100.0%; Score 101; DB 3; Length 826;
; Best Local Similarity 100.0%; Pred. No. 8.1e-08;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 DLDLEMLAPYIPMDDDFQL 19
DB      556 DLDLEMLAPYIPMDDDFQL 574

RESULT 21
US-09-148-547-2
; Sequence 2, Application US/09148547
; Patent No. 6124131
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
; FILE REFERENCE: 07265/151001
; CURRENT APPLICATION NUMBER: US/09/148,547
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-148-547-2
;
; Query Match      100.0%; Score 101; DB 3; Length 826;
; Best Local Similarity 100.0%; Pred. No. 8.1e-08;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 DLDLEMLAPYIPMDDDFQL 19
DB      556 DLDLEMLAPYIPMDDDFQL 574

RESULT 22
US-09-235-217-2
; Sequence 2, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.

; INFORMATION FOR SEQ ID NO: 2:
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 826 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-235-217-2
;
; Query Match      100.0%; Score 101; DB 3; Length 826;
; Best Local Similarity 100.0%; Pred. No. 8.1e-08;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 DLDLEMLAPYIPMDDDFQL 19
DB      556 DLDLEMLAPYIPMDDDFQL 574

RESULT 23
US-09-380-662-23
; Sequence 23, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-23
;
; Query Match      100.0%; Score 101; DB 3; Length 826;
; Best Local Similarity 100.0%; Pred. No. 8.1e-08;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 DLDLEMLAPYIPMDDDFQL 19
DB      556 DLDLEMLAPYIPMDDDFQL 574

RESULT 24
US-09-438-833-1
; Sequence 1, Application US/09438833
; Patent No. 643654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
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; VOLUME: 92
; PAGES: 5510-5514
; DATABASE ACCESSION NUMBER: GenBank U22431
; DATABASE ENTRY DATE: 1995-06-28
US-09-438-833-1

Query Match      100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
   |||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 25
US-09-702-705-330
; Sequence 330, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-330

Query Match      100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
   |||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 26
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lijun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match      100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
   |||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 27
US-09-383-581-2
; Sequence 2, Application US/09383581
; Patent No. 6562799
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/09/383,581
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-581-2

Query Match      100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
   |||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 28
US-09-614-124B-330
; Sequence 330, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-330

Query Match      100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 29
US-09-671-325-330
; Sequence 330, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-330

Query Match 100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 30
US-09-589-184-330
; Sequence 330, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-330

Query Match 100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 31
US-09-658-824-330
; Sequence 330, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-330

Query Match 100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 32
US-09-959-873B-18
; Sequence 18, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-873B-18

Query Match 100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||

```
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 33
US-09-949-016-6089
; Sequence 6089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6089
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6089

Query Match 100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 34
US-09-967-388-4
; Sequence 4, Application US/09967388
; Patent No. 6838430
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; WOUND HEALING
; FILE REFERENCE: UC077,001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match 100.0%; Score 101; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 35
PCT-US96-10251-2
; Sequence 2, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10251-2

Query Match 100.0%; Score 101; DB 5; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 36
US-09-919-039-149
; Sequence 149, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew E.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CD1
US-09-919-039-149

Query Match 100.0%; Score 101; DB 4; Length 827;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 37
US-09-972-784-5
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; Sequence 5, Application US/09972784

; Patent No. 6566088

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Bruik, Richard K.

; TITLE OF INVENTION: Poly(1-4-Hydroxylases

; FILE REFERENCE: UTSD0871

; CURRENT APPLICATION NUMBER: US/09/972,784

; CURRENT FILING DATE: 2001-10-04

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: sequence derived from HIF-a ODD domain.

US-09-972-784-5

Query Match

Best Local Similarity 88.1%; Score 89; DB 4; Length 19;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19

Db 1 DLDLEALAPYIPADDDFQL 19

RESULT 38

US-09-374-454-2

; Sequence 2, Application US/09374454

; Patent No. 6395548

; GENERAL INFORMATION:

; APPLICANT: Lee, Mu-En

; APPLICANT: Maemura, Koji

; APPLICANT: Hsieh, Chung-Ming

; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS

; FILE REFERENCE: 05433/037001

; CURRENT APPLICATION NUMBER: US/09/374,454

; CURRENT FILING DATE: 1999-08-13

; EARLIER APPLICATION NUMBER: US 60/096,515

; EARLIER FILING DATE: 1998-08-14

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-374-454-2

Query Match

Best Local Similarity 75.7%; Score 76.5; DB 3; Length 205;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAPYIPMD-DDFQL 19

Db 38 ELDLETLAPYIPMDGEDFQL 57

RESULT 39

US-08-785-241-4

; Sequence 4, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/785,241

; FILING DATE: 17-JAN-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UTSD:1229

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 870 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-785-241-4

Query Match

Best Local Similarity 75.7%; Score 76.5; DB 1; Length 870;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAPYIPMD-DDFQL 19

Db 523 ELDLETLAPYIPMDGEDFQL 542

RESULT 40

US-09-374-454-6

; Sequence 6, Application US/09374454

; Patent No. 6395548

; GENERAL INFORMATION:

; APPLICANT: Lee, Mu-En

; APPLICANT: Maemura, Koji

; APPLICANT: Hsieh, Chung-Ming

; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS

; FILE REFERENCE: 05433/037001

; CURRENT APPLICATION NUMBER: US/09/374,454

; CURRENT FILING DATE: 1999-08-13

; EARLIER APPLICATION NUMBER: US 60/096,515

; EARLIER FILING DATE: 1998-08-14

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 870

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-374-454-6

Query Match

Best Local Similarity 75.7%; Score 76.5; DB 3; Length 870;

Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAPYIPMD-DDFQL 19

Db 523 ELDLETLAPYIPMDGEDFQL 542

RESULT 41

US-08-785-241-5

; Sequence 5, Application US/08785241

; Patent No. 5695963

GENERAL INFORMATION:
APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
TITLE OF INVENTION: Endothelial PAS Domain Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,241
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1229
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-241-5

Query Match 75.7%; Score 76.5; DB 1; Length 875;
Best Local Similarity 80.0%; Pred. No. 0.0007;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAPYIPMD-DDFQL 19
:|||||:|||||:|||||
Db 523 ELDTLETAPYIPMDGEDFQL 542

RESULT 42
US-09-270-767-42631
Sequence 42631, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:

APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42631
LENGTH: 143
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-42631

Query Match 53.5%; Score 54; DB 4; Length 143;
Best Local Similarity 71.4%; Pred. No. 0.33;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MLAPYIPMDDDFQL 19
:|||||:|||||:|||||
Db 93 MRAPYIPIDDDMPL 106

RESULT 43
US-09-914-259-37
Sequence 37, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 1507
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-914-259-37

Query Match 53.5%; Score 54; DB 4; Length 1507;
Best Local Similarity 71.4%; Pred. No. 5.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MLAPYIPMDDDFQL 19
:|||||:|||||:|||||
Db 847 MRAPYIPIDDDMPL 860

RESULT 44
US-09-248-796A-20521
Sequence 20521, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20521
LENGTH: 182
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20521

Query Match 44.6%; Score 45; DB 4; Length 182;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MLAPYIPMDDD 16
:|||||:|||||:|||||
Db 44 MLAGYLPFDDDD 54

RESULT 45
US-09-959-873B-1
Sequence 1, Application US/09959873B
Patent No. 6787326
GENERAL INFORMATION:

APPLICANT: Ratcliffe, Peter John
APPLICANT: Maxwell, Patrick Henry
APPLICANT: Pugh, Christopher William
TITLE OF INVENTION: Interaction between the VHL Tumour
SUPPRESSOR AND HYPOXIA INDUCIBLE FACTOR, AND ASSAY METHODS
FILE REFERENCE: 3547.1000-000

; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-873B-1

Query Match 43.6%; Score 44; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LAPYIPMD 14
||| |||||
Db 1 LAPYIPMD 8

RESULT 46
US-09-543-681A-8077
; Sequence 8077, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8077
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8077

Query Match 43.6%; Score 44; DB 4; Length 98;
Best Local Similarity 75.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 EMLAPYIPMDDD 16
||| |||||
Db 87 ERLATLIPMDDD 98

RESULT 47
US-09-248-796A-15417
; Sequence 15417, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15417
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15417

Query Match 42.6%; Score 43; DB 4; Length 133;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMD 15
||| |||||
Db 95 DLLLSMKAPYITIDE 109

RESULT 48
US-09-489-039A-10142
; Sequence 10142, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10142
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10142

Query Match 42.6%; Score 43; DB 4; Length 820;
Best Local Similarity 61.1%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 2 LDLEMLAPYIPMDDDFQL 19
||| |||||
Db 498 LQLPALNPYIP--DDFTL 513

RESULT 49
US-09-959-873B-5
; Sequence 5, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-09-959-873B-5

Query Match 41.6%; Score 42; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LAPYIPMD 14
:|||||

Db 1 IAPYIPMD 8

RESULT 50

```

US-09-583-110-3221
; Sequence 3221, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3221
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3221

```

Query Match 41.6%; Score 42; DB 4; Length 650;
Best Local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY	3	DLEMLAPYIPMDDDFQ	18
		: : :	
Db	239	DFKFFAPALPLDDFFK	254

Search completed: February 9, 2005, 05:56:55
Job time : 20.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 105.667 Seconds
(without alignments)
69.544 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 101
Sequence: 1 DLDLEMLAPYIPMDDFOL 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	19	4	Aab49912 Human/mur
2	101	100.0	19	6	Aae30167 Peptide #
3	101	100.0	19	6	Aae30144 HIFalpha
4	101	100.0	19	6	Aae30162 Peptide #
5	101	100.0	19	6	Aae30172 Human HIF
6	101	100.0	19	6	Aae30158 HIF-lalaph
7	101	100.0	19	6	Abr82378 Hypoxia-i
8	101	100.0	19	8	Adp56728 Substrate
9	101	100.0	19	8	Adp79479 Hypoxia i
10	101	100.0	20	6	Abp55440 Hypoxia-i
11	101	100.0	20	8	Ado22337 HIF-lalaph
12	101	100.0	29	7	Aao23481 Murine HI
13	101	100.0	29	7	Aao23499 Murine HI
14	101	100.0	30	6	Abr82380 Hypoxia-i
15	101	100.0	34	4	Aab49913 Human/mur
16	101	100.0	34	6	Aae30161 Peptide #
17	101	100.0	34	6	Aae30151 HIFalpha
18	101	100.0	54	3	Aay94637 HIF-lalaph
19	101	100.0	54	7	Aao23490 Murine HI
20	101	100.0	54	7	Aao23530 Murine HI
21	101	100.0	54	7	Aao23528 Murine HI
22	101	100.0	54	7	Aao23529 Murine HI
23	101	100.0	116	3	Aay94632 HIF-lalaph
24	101	100.0	288	3	Aay94633 HIF-lalaph
25	101	100.0	301	3	Aay94634 HIF-lalaph

26	101	100.0	311	3	AAy94631	HIF-lalaph
27	101	100.0	409	8	ADO39389	Chimeric
28	101	100.0	444	4	AAB68415	Amino aci
29	101	100.0	466	8	ADO39390	Chimeric
30	101	100.0	538	8	ADO39387	Chimeric
31	101	100.0	542	5	ABP41474	Human ova
32	101	100.0	595	8	ADO39388	Chimeric
33	101	100.0	613	3	AAy94630	HIF-lalaph
34	101	100.0	613	5	AAU77614	Human hyp
35	101	100.0	632	8	ADO39391	Chimeric
36	101	100.0	652	3	AAy94629	HIF-lalaph
37	101	100.0	669	3	AAy84167	A variant
38	101	100.0	697	3	AAy84166	A variant
39	101	100.0	701	3	AAy84173	A variant
40	101	100.0	710	3	AAy84172	A variant
41	101	100.0	724	3	AAy84171	A variant
42	101	100.0	735	6	ABR82375	Hypoxia-i
43	101	100.0	735	8	ADN75066	Human hyp
44	101	100.0	749	3	AAy84170	A variant
45	101	100.0	756	3	AAy94635	HIF-lalaph
46	101	100.0	789	3	AAy84169	A variant
47	101	100.0	789	6	ADA18535	Human hyp
48	101	100.0	789	6	ADA18533	Human hyp
49	101	100.0	789	6	ADA18534	Human hyp
50	101	100.0	805	2	AAW06558	Hypoxia i
51	101	100.0	810	5	ABB57270	Mouse lac
52	101	100.0	813	3	AAy94636	HIF-lalaph
53	101	100.0	823	6	ABR41951	Rat hypox
54	101	100.0	825	7	ADD44855	Rat Prote
55	101	100.0	826	2	AAW06557	Human hyp
56	101	100.0	826	2	AAW80418	Amino aci
57	101	100.0	826	2	AAy06289	Human tra
58	101	100.0	826	3	AAy69407	A wild ty
59	101	100.0	826	3	AAy94640	Human hyp
60	101	100.0	826	4	AAy76854	Human lun
61	101	100.0	826	5	AAU85509	Clone #19
62	101	100.0	826	5	AAU77620	Human hyp
63	101	100.0	826	5	AAU77602	Human hyp
64	101	100.0	826	5	AAU77619	Human hyp
65	101	100.0	826	5	AAU77618	Human hyp

ALIGNMENTS

RESULT 1	
AAB49912	AAb49912 standard; peptide; 19 AA.
ID	AC
XX	AC AAB49912;
XX	DT 06-MAR-2001 (first entry)
XX	DE Human/murine HIF-lalaph subunit conserved motif #8.
XX	Mouse; human; HIF-lalaph; von Hippel-Lindau syndrome protein; VHL;
XX	hypoxia inducible factor-1; cancer; ischaemia.
XX	Mus sp.
XX	Homo sapiens.
XX	WO200069908-A1.
XX	PD 23-NOV-2000.
XX	PF 12-MAY-2000; 2000WO-GB001826.
XX	PR 12-MAY-1999; 95GB-00011047.
XX	PA (ISIS-) ISIS INNOVATION LTD.
XX	PI Ratcliffe PJ, Maxwell PH, Pugh CW;
XX	

DR WPI; 2001-025006/03.

XX Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha

PT subunit interaction modulators for treating ischemia by contacting a VHL

PT protein and an HIF subunit protein with a putative modulator.

XX Claim 13; Page 49; 56pp; English.

XX The present invention describes a novel assay for use in identifying

CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible

CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises

CC contacting the VHL protein, the HIF-1alpha subunit and the putative

CC modulator under conditions where the former two would normally complex.

CC Modulators of this type are useful in the treatment of cancer and

CC ischaemic conditions such as coronary, cerebral and vascular

CC insufficiency

XX Sequence 19 AA;

Query Match 100.0%; Score 101; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.8e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2

AAE30167

ID AAE30167 standard; peptide; 19 AA.

AC AAE30167;

XX Peptide #7 used to block HIF-1alpha/pVHL interaction.

DE Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.

KW Unidentified.

OS WO200274981-A2.

XX 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

PR 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

PA Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

XX WPI; 2003-018808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,

PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,

PT cancer, or inflammatory disorders.

XX Example 1; Page 247; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor

CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and

CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of

CC the invention are used for treating conditions such as ischaemia, wound

CC healing, auto-, allo-, and xeno-transplantation, systemic high blood

CC pressure, cancer, or inflammatory disorders. They are useful in anti-

CC sense regulation of the HIF hydroxylase activity and in particular HIF

CC prolyl hydroxylase activity within a cell. They are also used to identify

CC additional substrates of HIF hydroxylases. Sequences of the invention are

CC used as therapeutic agents and in purification, isolation, or screening

CC methods involving immuno-precipitation techniques and for detecting

CC polypeptides in biological samples. The invention is useful in gene

CC therapy. The present sequence is HIF1alpha subunit antagonist. This

CC used to design double stranded RNAs for use in RNA interference. They are

CC methods as therapeutic agents and in purification, isolation, or screening

CC polypeptides in biological samples. The invention is useful in gene

CC interaction. This sequence is used in the invention

XX Sequence 19 AA;

Query Match 100.0%; Score 101; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.8e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

DB 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 3

AAE30144

ID AAE30144 standard; peptide; 19 AA.

AC AAE30144;

XX 24-FEB-2003 (first entry)

DE HIF1alpha subunit antagonist #1.

XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;

KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;

KW antagonist.

XX Unidentified.

OS Key Location/Qualifiers

FH Modified-site 2 /label= Hyp

FT WO200274981-A2.

XX 26-SEP-2002.

XX 21-MAR-2002; 2002WO-GB001381.

XX 21-MAR-2001; 2001GB-00007123.

PR 02-AUG-2001; 2001GB-00018952.

XX (ISIS-) ISIS INNOVATION LTD.

PA Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

XX WPI; 2003-018808/01.

XX Novel isolated polypeptide useful for treating ischemia, wound healing,

PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,

PT cancer, or inflammatory disorders.

XX Claim 49; Page 196; 256pp; English.

XX The invention relates to polypeptides having hypoxia inducible factor

CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and

CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of

CC the invention are used for treating conditions such as ischaemia, wound

CC healing, auto-, allo-, and xeno-transplantation, systemic high blood

CC pressure, cancer, or inflammatory disorders. They are useful in anti-

CC sense regulation of the HIF hydroxylase activity and in particular HIF

CC prolyl hydroxylase activity within a cell. They are also used to identify

CC additional substrates of HIF hydroxylases. Sequences of the invention are

```

CC sequence is used in the invention
XX
SQ Sequence 19 AA;

    Query Match          100.0%; Score 101; DB 6; Length 19;
    Best Local Similarity 100.0%; Pred. No. 3.8e-09;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFOL 19
   |||||
Db 1 DLDLEMLAPYIPMDDDFOL 19

RESULT 4
AAE30162
ID AAE30162 standard; peptide; 19 AA.
XX
AC AAE30162;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #2 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS Unidentified.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX WPI; 2003-018808/01.
XX
DR Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 246; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC methods involving immuno-precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;

    Query Match          100.0%; Score 101; DB 6; Length 19;
    Best Local Similarity 100.0%; Pred. No. 3.8e-09;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFOL 19
   |||||
Db 1 DLDLEMLAPYIPMDDDFOL 19

RESULT 6
AAE30158
ID AAE30158 standard; peptide; 19 AA.
XX
AC AAE30158;
XX
Qy 1 DLDLEMLAPYIPMDDDFOL 19
   |||||
Db 1 DLDLEMLAPYIPMDDDFOL 19

RESULT 5
AAE30172
ID AAE30172 standard; peptide; 19 AA.
XX
AC AAE30172;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human HIF1-alpha peptide #2.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW human; HIF1-alpha.
XX
OS Homo sapiens.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX WPI; 2003-018808/01.
XX
DR Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Disclosure; Page 252; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1.2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno-precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is human HIF1-alpha peptide. This sequence
CC is used in the invention
XX
SQ Sequence 19 AA;

    Query Match          100.0%; Score 101; DB 6; Length 19;
    Best Local Similarity 100.0%; Pred. No. 3.8e-09;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFOL 19
   |||||
Db 1 DLDLEMLAPYIPMDDDFOL 19

RESULT 6
AAE30158
ID AAE30158 standard; peptide; 19 AA.
XX
AC AAE30158;
XX
Qy 1 DLDLEMLAPYIPMDDDFOL 19
   |||||
Db 1 DLDLEMLAPYIPMDDDFOL 19

```

DT 24-FEB-2003 (first entry)
 XX HIF-1alpha pVHL minimal binding domain.
 XX Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
 KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
 KW human.
 XX Homo sapiens.
 OS
 FN WO200274981-A2.
 PD 26-SEP-2002.
 XX
 PF 21-MAR-2002; 2002WO-GB001381.
 XX
 PR 21-MAR-2001; 2001GB-00007123.
 PR 02-AUG-2001; 2001GB-00018952.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
 PI WPI; 2003-018808/01.
 DR
 XX Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.
 XX
 PS Example 1; Page 245; 256pp; English.
 XX
 CC The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is HIF-1alpha pVHL minimal binding domain.
 CC This sequence is used in the invention
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 101; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 7
 ABR82378
 ID ABR82378 standard; peptide; 19 AA.
 XX
 AC ABR82378;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Hypoxia-inducible factor 1 (HIF-1) alpha peptide inhibitor.
 XX
 KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
 KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
 KW tranquilizer; vulnary; cardiant; cerebroprotective; angiogenesis.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 9
 FT /label= Hyp
 FT /note= "hydroxyproline"
 XX
 XX WO2003057820-A2.
 FN
 PD 17-JUL-2003.
 XX
 XX 04-OCT-2002; 2002WO-US031699.
 XX
 XX 21-DEC-2001; 2001US-00032361.
 PR
 XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 PA
 PI Mcgrath K;
 XX
 DR WPI; 2003-645988/61.
 XX
 PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
 PT ubiquitination, and activator of vascular endothelial growth factor
 PT transcription useful for treating tissue injuries including wounds,
 PT surgical incisions.
 XX
 XX Claim 2; Page 8; 37pp; English.
 PS
 CC The invention relates to peptide inhibitors of hypoxia-inducible factor
 CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
 CC transcription of erythropoietin (EPO), vascular endothelial growth factor
 CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
 CC for treating tissue injuries including wounds, surgical incisions,
 CC chronic wounds, heart disease and stroke. The present sequence represents
 CC a specific example of HIF-1 alpha peptide inhibitor, containing the
 CC oxygen-dependent degradation sequence of HIF-1 alpha
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 101; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 Db 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 8
 ADP56728
 ID ADP56728 standard; peptide; 19 AA.
 XX
 AC ADP56728;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Substrate peptide used in human HIF prolyl hydroxylase screening assay.
 XX
 KW fat metabolism; HIFalpha; hypoxia inducible factor alpha subunit;
 KW atherosclerosis; diabetes; obesity; HIF prolyl hydroxylase substrate;
 KW human; HIF-PH.
 XX
 OS Homo sapiens.
 XX
 FN WO2004052285-A2.
 PD 24-JUN-2004.
 XX
 XX 05-DEC-2003; 2003WO-US038690.
 PF
 XX 06-DEC-2002; 2002US-0431351P.
 PR
 PR 06-JUN-2003; 2003US-0476331P.
 PR 06-JUN-2003; 2003US-0476726P.
 PR 04-DEC-2003; 2003US-00729167.

XX (FIBR-) FIBROGEN INC.
 XX Fournay PD, Guenzler-Pukall V, Klaus SJ, Lin AY, Neff TB;
 PI Seeley TW;
 XX WPI; 2004-468689/44.
 DR
 XX Regulating fat metabolism or fat metabolic process in subjects, by
 PT stabilizing human foreskin fibroblasts alpha in subject, thus regulating
 PT fat metabolism or fat metabolic process in subject.
 XX
 PS Example 9; SEQ ID NO 1; 66pp; English.
 XX
 CC The invention relates to a novel method for regulating fat metabolism or
 CC the fat metabolic process in a subject which comprises stabilising human
 CC foreskin fibroblast HIFalpha (hypoxia inducible factor alpha subunit) in
 CC the subject, or administering a compound that inhibits HIF hydroxylase
 CC activity, thus regulating fat metabolism or the fat metabolic process in
 CC the subject. The method of the invention may be useful for regulating fat
 CC metabolism or a fat metabolic process in a subject. The subject is an
 CC animal, preferably a mammal, more preferably human and the method is
 CC performed in a human cell, tissue or organ. The method may be useful for
 CC treating or preventing atherosclerosis, diabetes and obesity in a
 CC subject. The current sequence is that of the substrate peptide of the
 CC invention which is used during a screening assay of human HIF prolyl
 CC hydroxylase (HIF-PH).
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 101; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 9
 ID ADP79479 standard; peptide; 19 AA.
 XX
 AC ADP79479;
 XX
 DT 04-NOV-2004 (first entry)
 DE Hypoxia inducible factor prolyl hydroxylase substrate peptide.
 XX
 KW Human; Hypoxia inducible factor prolyl hydroxylase; glucose metabolism;
 KW antidiabetic; anorectic; hypotensive; antilipaeamic; nephrotropic;
 KW neuroprotective; ophthalmological; antiarteriosclerotic; vasotropic;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX
 FN WO2004052284-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 05-DEC-2003; 2003WO-US038689.
 XX
 PR 06-DEC-2002; 2002US-0431351P.
 PR 06-JUN-2003; 2003US-047631P.
 PR 06-JUN-2003; 2003US-0478726P.
 PR 04-DEC-2003; 2003US-00729704.
 XX
 PA (FIBR-) FIBROGEN INC.
 XX
 PI Guenzler-Pukall V, Klaus SJ, Langsetmo Parobok I, Seeley TW;
 XX WPI; 2004-468689/44.
 DR

PT Regulating glucose metabolism or glucose metabolic process in subject,
 PT involves stabilizing hypoxia inducible factor alpha in subject, or
 PT administering to subject compound inhibiting hypoxia inducible factor
 PT hydroxylase activity.
 XX
 PS Example 14; SEQ ID NO 5; 74pp; English.
 XX
 CC The present sequence is that of a substrate peptide for hypoxia inducible
 CC factor (HIF) prolyl hydroxylase. It was used in an example from the
 CC invention for the identification of compounds useful for HIF alpha
 CC stabilisation. The invention provides methods and compounds for
 CC regulating glucose metabolism by stabilising HIF alpha, especially by
 CC administering a compound that inhibits HIF hydroxylase activity. The
 CC method of stabilising HIF alpha is used in claimed methods for achieving
 CC glucose homeostasis, decreasing blood glucose levels, decreasing glycated
 CC haemoglobin levels, altering expression of a glucose regulatory factor,
 CC altering expression of a glycolytic factor, treating or preventing
 CC diabetes, treating or preventing a disorder associated with increased
 CC blood glucose levels (especially diabetes, hyperglycaemia, obesity,
 CC hypertension, hyperlipidaemia, nephropathy, neuropathy, retinopathy,
 CC impaired glucose tolerance, atherosclerosis and vascular disease),
 CC treating or preventing a condition associated with diabetes, decreasing
 CC blood triglyceride levels, reducing insulin resistance, and increasing
 CC glycaemic control in a subject.
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 101; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 1 DLDLEMLAPYIPMDDDFQL 19
 RESULT 10
 ID ABP55440 standard; peptide; 20 AA.
 XX
 AC ABP55440;
 XX
 DT 05-FEB-2003 (first entry)
 DE Hypoxia-inducible factor (HIF) 1 alpha peptide.
 XX
 KW Hypoxia; hypoxia-inducible factor; HIF1-alpha; hypoxic-related disorder;
 KW ischaemic-related disorder; hypoxia-inducible factor-related disorder;
 KW prolyl hydroxylase; HIF; hypoxic; ischaemic; vasotropic; cardiant;
 KW cerebroprotective; cytostatic; thrombolytic; antidiabetic; nephrotropic;
 KW myocardial infarction; heart disease; stroke; cancer; diabetes;
 KW cell-proliferating disorder; deep vein thrombosis; pulmonary embolus;
 KW renal failure; angiogenesis; vascularisation; prolyl hydroxylase.
 XX
 OS Homo sapiens.
 XX
 FN WO200274249-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-MAR-2002; 2002WO-US008886.
 XX
 PR 20-MAR-2001; 2001US-0277425P.
 PR 20-MAR-2001; 2001US-0277431P.
 PR 20-MAR-2001; 2001US-0277440P.
 PR 09-NOV-2001; 2001US-032334P.
 PR 09-NOV-2001; 2001US-0332493P.
 PR 09-NOV-2001; 2001US-0345200P.
 PR 20-DEC-2001; 2001US-0342598P.

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PR 20-DEC-2001; 2001US-0345131P.
PR 20-DEC-2001; 2001US-0345132P.
PR 19-MAR-2002; 2002US-00101812.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Kaelin WG, Ivan M;
XX
XX WPI; 2003-058330/05.
XX
XX Treating or preventing a hypoxic- or ischemic-related disorder, e.g.
XX myocardial infarction, stroke, cancer, thrombosis or renal failure, by
XX administering a modulator prolyl hydroxylation of hypoxia-inducible
XX factor (HIF).
XX
XX Disclosure; Page 26; 128pp; English.
XX
CC The present invention describes a method for treating or preventing a
CC hypoxic-related disorder, ischaemic-related disorder, or hypoxia-
CC inducible factor (HIF)-related disorder in a subject by administering to
CC the subject a compound that modulates prolyl hydroxylation of HIF, such
CC that the hypoxic-, ischaemic-, or HIF-related disorder is treated,
CC prevented, reversed or stabilised. HIF-related sequences can have
CC vasotropic, cardiant, cerebroprotective, cytosstatic, thrombolytic,
CC antidiabetic, and nephrotropic activities. The method is useful for
CC treating hypoxia-related disorder, ischaemic-related disorder or HIF-
CC related disorder. In particular, the hypoxic- or ischaemic-related
CC disorder is an acute event (e.g. myocardial infarction, heart disease,
CC stroke, cancer or cell-proliferating disorder, or diabetes) or a chronic
CC event (e.g. deep vein thrombosis, pulmonary embolus or renal failure),
CC especially a chronic event not caused by tissue scarring. The method is
CC also useful for increasing angiogenesis or vascularisation. The present
CC sequence represents a human hypoxia-inducible factor 1 alpha (HIF1-alpha)
CC peptide which is given in the exemplification of the present invention
XX
XX Sequence 20 AA;
XX
XX Query Match 100.0%; Score 101; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4e-09;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 DLDLEMLAPYIPMDDDFOL 19
XX | | | | | | | | | | | | | | | | |
XX Db 1 DLDLEMLAPYIPMDDDFOL 19
XX
XX RESULT 11
XX ID ADO22337 standard; peptide; 20 AA.
XX AC ADO22337;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE HIF-1alpha ligand binding site peptide SEQ ID NO:15.
XX
XX transgenic non-human animal; light-generating fusion protein;
XX ligand binding site; light-generating polypeptide moiety;
XX hypoxia-inducible factor 1 alpha; HIF-1alpha; hypoxic tissue;
XX respiratory; cytosstatic; vasotropic; virucide; hypoxic condition; cancer;
XX ischaemia; viral infection; drug screening; drug discovery;
XX ligand binding site peptide.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO2004042361-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US035154.
XX
XX 04-NOV-2002; 2002US-00287670.
XX
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Kaelin WG, Livingston DM, Kim T;
XX
XX WPI; 2004-400725/37.
XX
XX New transgenic non-human animal comprising light-generating fusion
XX protein, useful in diagnosing and treating hypoxic conditions, cancer,
XX ischemia and viral infections and in drug screening and discovery.
XX
XX Disclosure; SEQ ID NO 15; 111pp; English.
XX
XX The present invention describes a transgenic non-human animal comprising
XX a recombinant nucleic acid molecule stably integrated into the genome of
XX the animal, where the molecule encodes a light-generating fusion protein
XX comprising a ligand binding site and a light-generating polypeptide
XX moiety. Also described: (1) an isolated cell of the animal; (2) producing
XX a transgenic non-human animal; (3) identifying a compound capable of
XX modifying an activity of hypoxia-inducible factor (HIF) 1 alpha; and (4)
XX detecting hypoxic tissue. The compound has respiratory, cytosstatic,
XX vasotropic and virucide activities. The transgenic non-human animal,
XX light-generating fusion protein, agents, kits and compositions are useful
XX in diagnosing and treating hypoxic conditions, cancer, ischaemia and
XX viral infections and in drug screening and discovery. The present
XX sequence represents a HIF-1alpha ligand binding site peptide, which is
XX used in the exemplification of the present invention.
XX
XX Sequence 20 AA;
XX
XX Query Match 100.0%; Score 101; DB 8; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4e-09;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 DLDLEMLAPYIPMDDDFOL 19
XX | | | | | | | | | | | | | | | | |
XX Db 1 DLDLEMLAPYIPMDDDFOL 19
XX
XX RESULT 12
XX ID AAO23481 standard; peptide; 29 AA.
XX AC AAO23481;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Murine HIF-1alpha protein mutant fragment.
XX
XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
XX ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
XX antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
XX mutant.
XX
XX Mus sp.
XX OS
XX WO2003074560-A2.
XX
XX 12-SEP-2003.
XX
XX 05-MAR-2003; 2003WO-SE000372.
XX
XX 05-MAR-2002; 2002US-0361333P.
XX
XX 27-NOV-2002; 2002US-0429307P.
XX
XX (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
XX Pereira T, Poellinger L, Hellstroem M;
XX
XX WPI; 2003-712876/67.
XX
XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
XX angiogenesis, or treating a condition associated with HIF-1alpha
XX

```

PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 XX Claim 39; Page 93; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a specific example
 CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-
 CC related conditions
 XX
 XX Sequence 29 AA;
 SQ
 Query Match 100.0%; Score 101; DB 7; Length 29;
 Best Local Similarity 100.0%; Pred. No. 6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 10 DLDLEMLAPYIPMDDDFQL 28
 RESULT 13
 AAO23499
 ID AAO23499 standard; peptide; 29 AA.
 AC AAO23499;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX Murine HIF-1alpha protein N-TAD region fragment (residues 546-573).
 DE
 XX HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD.
 XX
 XX Mus sp.
 OS
 XX WO2003074560-A2.
 PN
 XX 12-SEP-2003.
 PD
 XX 05-MAR-2003; 2003WO-SE000372.
 PF
 XX 05-MAR-2002; 2002US-036133P.
 PR
 XX 27-NOV-2002; 2002US-0429307P.
 PR
 XX (ANGI-) ANGIOGENETICS SWEDEN AB.
 PA
 XX Pereira T, Poellinger L, Hellstroem M;
 PI
 XX WPI; 2003-712876/67.
 DR
 XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 PT
 XX Example 6; Fig 19; 96pp; English.
 PS
 XX

CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein
 XX
 XX Sequence 29 AA;
 SQ
 Query Match 100.0%; Score 101; DB 7; Length 29;
 Best Local Similarity 100.0%; Pred. No. 6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 10 DLDLEMLAPYIPMDDDFQL 28
 RESULT 14
 ABR82380
 ID ABR82380 standard; peptide; 30 AA.
 XX
 XX ABR82380;
 AC
 XX 06-NOV-2003 (first entry)
 DT
 XX Hypoxia-inducible factor 1 (HIF-1) alpha inhibitor ODD peptide.
 DE
 XX HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
 KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
 KW tranquilizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 20
 FT /label= Hyp
 FT /note= "hydroxyproline"
 FT
 XX WO2003057820-A2.
 PN
 XX 17-JUL-2003.
 PD
 XX 04-OCT-2002; 2002WO-US031699.
 PF
 XX 21-DEC-2001; 2001US-00032361.
 PR
 XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 PA
 XX Mcgrath K;
 PI
 XX WPI; 2003-645988/61.
 DR
 XX Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
 PT ubiquitination, and activator of vascular endothelial growth factor
 PT transcription useful for treating tissue injuries including wounds,
 PT surgical incisions.
 PT
 XX Claim 2; Page 9; 37pp; English.
 PS
 XX The invention relates to peptide inhibitors of hypoxia-inducible factor
 CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
 CC transcription of erythropoietin (EPO), vascular endothelial growth factor

CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC an ODD peptide, a specific example of HIF-1 alpha peptide inhibitor,
CC containing the oxygen-dependent degradation sequence of HIF-1 alpha
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 101; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 12 DLDLEMLAPYIPMDDDFQL 30

RESULT 15

AAB49913
ID AAB49913 standard; peptide; 34 AA.

XX AC AAB49913;

XX DT 06-MAR-2001 (first entry)

XX DE Human/murine HIF-1alpha subunit conserved motif #9.

XX KW Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
XX KW hypoxia inducible factor-1; cancer; ischaemia.

XX OS Mus sp.

XX OS Homo sapiens.

XX FN WO200069908-A1.

XX PD 23-NOV-2000.

XX PF 12-MAY-2000; 2000WO-GB001826.

XX PR 12-MAY-1999; 99GB-00011047.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Ratcliffe PJ, Maxwell PH, Pugh CW;

XX WPI; 2001-025006/03.

XX PT Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
XX PT subunit interaction modulators for treating ischemia by contacting a VHL
XX PT protein and an HIF subunit protein with a putative modulator.

XX PS Claim 14; Page 50; 56pp; English.

XX CC The present invention describes a novel assay for use in identifying
XX CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
XX CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
XX CC contacting the VHL protein, the HIF-1alpha subunit and the putative
XX CC modulator under conditions where the former two would normally complex.
XX CC Modulators of this type are useful in the treatment of cancer and
XX CC ischaemic conditions such as coronary, cerebral and vascular
XX CC insufficiency

XX SQ Sequence 34 AA;

Query Match

Best Local Similarity 100.0%; Score 101; DB 4; Length 34;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 16

AAE30161

ID AAE30161 standard; peptide; 34 AA.

XX AC AAE30161;

XX DT 24-FEB-2003 (first entry)

XX DE Peptide #1 used to block HIF-1alpha/pVHL interaction.

XX KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
XX KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.

XX OS Unidentified.

XX FN WO200274981-A2.

XX PD 26-SEP-2002.

XX PF 21-MAR-2002; 2002WO-GB001381.

XX PR 21-MAR-2001; 2001GB-00007123.

XX PR 02-AUG-2001; 2001GB-00018952.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;

XX WPI; 2003-018808/01.

XX DR Novel isolated polypeptide useful for treating ischemia, wound healing,
XX PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
XX PT cancer, or inflammatory disorders.

XX PS Example 1; Page 246; 256pp; English.

XX CC The invention relates to polypeptides having hypoxia inducible factor
XX CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
XX CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
XX CC the invention are used for treating conditions such as ischaemia, wound
XX CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
XX CC pressure, cancer, or inflammatory disorders. They are useful in anti-
XX CC sense regulation of the HIF hydroxylase activity and in particular HIF
XX CC additional substrates of HIF hydroxylases. Sequences of the invention are
XX CC used to design double stranded RNAs for use in RNA interference. They are
XX CC used as therapeutic agents and in purification, isolation, or screening
XX CC methods involving immuno-precipitation techniques and for detecting
XX CC polypeptides in biological samples. The invention is useful in gene
XX CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
XX CC interaction. This sequence is used in the invention

XX SQ Sequence 34 AA;

Query Match

Best Local Similarity 100.0%; Score 101; DB 6; Length 34;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 17

AAE30151

ID AAE30151 standard; peptide; 34 AA.

XX AC AAE30151;

XX DT 24-FEB-2003 (first entry)

XX DE HIFalpha subunit antagonist #8.

XX XX

KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
 KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
 KW antagonist.
 OS Unidentified.
 XX
 XX WO200274981-A2.
 PN
 XX
 XX 26-SEP-2002.
 PD
 XX
 XX 21-MAR-2002; 2002WO-GB001381.
 PF
 XX
 XX 21-MAR-2001; 2001GB-00007123.
 PR
 XX 02-AUG-2001; 2001GB-00018952.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX
 XX Maxwell PH., Pugh CW, Ratcliffe PJ, Schofield CJ;
 PI
 XX WPI; 2003-018808/01.
 DR
 XX
 XX Novel isolated polypeptide useful for treating ischemia, wound healing,
 PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
 PT cancer, or inflammatory disorders.
 PT
 XX
 XX Disclosure; Page 239; 256pp; English.
 PS
 XX
 XX The invention relates to polypeptides having hypoxia inducible factor
 CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
 CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
 CC the invention are used for treating conditions such as ischaemia, wound
 CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
 CC pressure, cancer, or inflammatory disorders. They are useful in anti-
 CC sense regulation of the HIF hydroxylase activity and in particular HIF
 CC prolyl hydroxylase activity within a cell. They are also used to identify
 CC additional substrates of HIF hydroxylases. Sequences of the invention are
 CC used to design double stranded RNAs for use in RNA interference. They are
 CC used as therapeutic agents and in purification, isolation, or screening
 CC methods involving immuno-precipitation techniques and for detecting
 CC polypeptides in biological samples. The invention is useful in gene
 CC therapy. The present sequence is HIFalpha subunit antagonist. This
 CC sequence is used in the invention
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 101; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 Db 8 DLDLEMLAPYIPMDDDFQL 26
 |||||
 RESULT 18
 AAY94637
 ID AAY94637 standard; protein; 54 AA.
 XX
 AC AAY94637;
 XX
 XX 15-AUG-2000 (first entry)
 DT
 XX
 XX HIF-1alpha variant protein sequence HIF-1alpha/531-584.
 DE
 XX
 KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX
 XX Homo sapiens.
 OS
 XX WO200029437-A1.
 PN
 XX 25-MAY-2000.
 PR
 XX

PF 11-NOV-1999; 99WO-SB002053.
 XX
 PR 13-NOV-1998; 98SE-00003891.
 XX
 XX (PHAA) PHARMACIA & UPJOHN AB.
 PA
 XX Berkenstam A, Poellinger L;
 PI
 XX WPI; 2000-399715/34.
 DR
 XX
 XX Human hypoxia-inducible factor alpha variants for identifying compounds
 PT that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 PT
 XX
 PS Claim 19; Page 84-85; 87pp; English.
 XX
 XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of HIF-
 CC angiogenesis, erythropoiesis an glycolysis
 CC
 XX Sequence 54 AA;
 Query Match 100.0%; Score 101; DB 3; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 Db 26 DLDLEMLAPYIPMDDDFQL 44
 |||||
 RESULT 19
 AAO23490
 ID AAO23490 standard; peptide; 54 AA.
 XX
 AC AAO23490;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX
 XX Murine HIF-1alpha protein N-TAD region fragment (residues 531-584) .
 DE
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD.
 XX
 XX Mus sp.
 OS
 XX WO2003074560-A2.
 PN
 XX 12-SEP-2003.
 PD
 XX
 XX 05-MAR-2003; 2003WO-SE000372.
 PF
 XX 05-MAR-2002; 2002US-0361333P.
 PR
 XX 27-NOV-2002; 2002US-0429307P.
 PR
 XX

PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX
 PI Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX

PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 XX angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX

PS Example 4; Fig 4; 96pp; English.
 XX

CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia; or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein
 XX

SQ Sequence 54 AA;
 Query Match 100.0%; Score 101; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 25 DLDLEMLAPYIPMDDDFQL 43
 |||||
 |||||

RESULT 20
 ID AAO23530 standard; peptide; 54 AA.
 XX
 AC AAO23530;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Murine HIF-1alpha protein N-TAD region mutant fragment 0572A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 XX
 PR 27-NOV-2002; 2002US-0429307P.
 XX

(ANGI-) ANGIOGENETICS SWEDEN AB.
 PA Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX

PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 XX angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX

PS Example 11; Fig 27; 96pp; English.
 XX

CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia; or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX

SQ Sequence 54 AA;
 Query Match 100.0%; Score 101; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 25 DLDLEMLAPYIPMDDDFQL 43
 |||||
 |||||

RESULT 21
 ID AAO23528 standard; peptide; 54 AA.
 XX
 AC AAO23528;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Murine HIF-1alpha protein N-TAD region mutant fragment L573A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
 KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 XX
 PR 27-NOV-2002; 2002US-0429307P.
 XX

(ANGI-) ANGIOGENETICS SWEDEN AB.
 PA Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX

PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 XX angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX

PS Example 11; Fig 27; 96pp; English.
 XX

XX The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX Sequence 54 AA;
 SQ

Query Match 100.0%; Score 101; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
 Db 25 DLDLEMLAPYIPMDDDFQL 43
 |||||

RESULT 22
 AAO23529
 ID AAO23529 standard; peptide; 54 AA.
 XX
 AC AAO23529;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Murine HIF-1alpha protein N-TAD region mutant fragment QR-A.
 XX
 KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
 KW ophthalmological; antiinflammatory; cardiac; antirheumatic; mouse;
 KW antarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
 KW N-TAD; mutant.
 XX
 OS Mus sp.
 XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 PR 27-NOV-2002; 2002US-0429307P.
 XX
 PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX
 PI Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX
 XX New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 PS Example 11; Fig 27; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or

CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
 CC within the N-TAD region of a murine HIF-1 alpha protein
 XX Sequence 54 AA;
 SQ

Query Match 100.0%; Score 101; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
 Db 25 DLDLEMLAPYIPMDDDFQL 43
 |||||

RESULT 23
 AAY94632
 ID AAY94632 standard; protein; 116 AA.
 XX
 AC AAY94632;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE HIF-1alpha variant protein sequence HIF-1alpha/526-641.
 XX
 KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200029437-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 11-NOV-1999; 99WO-SE002053.
 XX
 PR 13-NOV-1998; 98SE-00003891.
 XX
 PA (PHAA) PHARMACIA & UPJOHN AB.
 XX
 PI Berkenstam A, Poellinger L;
 XX
 DR WPI; 2000-399715/34.
 XX
 XX Human hypoxia-inducible factor alpha variants for identifying compounds
 PT that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 XX
 PS Claim 13; Page 76-77; 87pp; English.
 XX
 CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the

CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis and glycolysis

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 101; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 24
AAAY94633
ID AAY94633 standard; protein; 288 AA.

XX AC AAY94633;

DT 15-AUG-2000 (first entry)

XX DE HIF-1alpha variant protein sequence HIF-1alpha/526-813.

XX KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
XX KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX OS Homo sapiens.

XX PN WO200029437-A1.

XX PD 25-MAY-2000.

XX PF 11-NOV-1999; 99WO-SE002053.

XX PR 13-NOV-1998; 98SE-00003891.

XX PA (PHAA) PHARMACIA & UPJOHN AB.

XX PI Berkenstam A, Poellinger L;

XX DR WPI; 2000-399715/34.

XX PT Human hypoxia-inducible factor alpha variants for identifying compounds
XX PT that modulate its functional domain and regulate genes involved in
XX PT angiogenesis, erythropoiesis.

XX PS Claim 13; Page 77-78; 87pp; English.

XX CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX CC multi-step process which includes hypoxia-dependent nuclear import and
XX CC activation of the transactivation domain. The HIF-1alpha consists of a
XX CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX CC nuclear localization sequence located at amino acids 718-584, a
XX CC transactivator domain (N-TAD) located between amino acids 531 and 584,
XX CC and a second transactivator domain (C-TAD) located between 813 and 826.
XX CC The invention relates to isolated variants of HIF-1alpha, such as that
XX CC represented by the present sequence. The variants are useful for
XX CC identifying compounds capable of modulating the function of a functional
XX CC domain of human HIF-1alpha. The method comprises contacting a candidate
XX CC compound with a cell expressing a HIF-1alpha variant conjugated to a
XX CC molecular probe. The localization of the probe can be detected in the
XX CC cell. The Aequorea victoria green fluorescent protein can be used as the
XX CC molecular probe. The compounds are useful for the regulation of HIF-
XX CC 1alpha target genes, such as those involved in the regulation of
XX CC angiogenesis, erythropoiesis and glycolysis

XX SQ Sequence 288 AA;

Query Match 100.0%; Score 101; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 25
AAAY94634
ID AAY94634 standard; protein; 301 AA.

XX AC AAY94634;

DT 15-AUG-2000 (first entry)

XX DE HIF-1alpha variant protein sequence HIF-1alpha/526-826.

XX KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
XX KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX OS Homo sapiens.

XX PN WO200029437-A1.

XX PD 25-MAY-2000.

XX PF 11-NOV-1999; 99WO-SE002053.

XX PR 13-NOV-1998; 98SE-00003891.

XX PA (PHAA) PHARMACIA & UPJOHN AB.

XX PI Berkenstam A, Poellinger L;

XX DR WPI; 2000-399715/34.

XX PT Human hypoxia-inducible factor alpha variants for identifying compounds
XX PT that modulate its functional domain and regulate genes involved in
XX PT angiogenesis, erythropoiesis.

XX PS Claim 13; Page 78-79; 87pp; English.

XX CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX CC multi-step process which includes hypoxia-dependent nuclear import and
XX CC activation of the transactivation domain. The HIF-1alpha consists of a
XX CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX CC nuclear localization sequence located at amino acids 718-584, a
XX CC transactivator domain (N-TAD) located between amino acids 531 and 584,
XX CC and a second transactivator domain (C-TAD) located between 813 and 826.
XX CC The invention relates to isolated variants of HIF-1alpha, such as that
XX CC represented by the present sequence. The variants are useful for
XX CC identifying compounds capable of modulating the function of a functional
XX CC domain of human HIF-1alpha. The method comprises contacting a candidate
XX CC compound with a cell expressing a HIF-1alpha variant conjugated to a
XX CC molecular probe. The localization of the probe can be detected in the
XX CC cell. The Aequorea victoria green fluorescent protein can be used as the
XX CC molecular probe. The compounds are useful for the regulation of HIF-
XX CC 1alpha target genes, such as those involved in the regulation of
XX CC angiogenesis, erythropoiesis and glycolysis

XX SQ Sequence 301 AA;

Query Match 100.0%; Score 101; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 31 DLDLEMLAPYIPMDDDFQL 49

```
RESULT 26
AA94631
ID AAY94631 standard; protein; 311 AA.
XX AC AAY94631;
XX DT 15-AUG-2000 (first entry)
XX DE HIF-1alpha variant protein sequence HIF-1alpha/331-641.
XX KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
XX regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX OS Homo sapiens.
XX PN WO200029437-A1.
XX PD 25-MAY-2000.
XX PF 11-NOV-1999; 99WO-SE002053.
XX PR 13-NOV-1998; 98SE-00003891.
XX PA (PHAA ) PHARMACIA & UPJOHN AB.
XX PI Berkenstam A, Poellinger L;
XX WPI; 2000-399715/34.
XX Human hypoxia-inducible factor alpha variants for identifying compounds
XX that modulate its functional domain and regulate genes involved in
XX angiogenesis, erythropoiesis.
XX Claim 13; Page 74-75; 87pp; English.
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX multi-step process which includes hypoxia-dependent nuclear import and
XX activation of the transactivation domain. The HIF-1alpha consists of a
XX number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX nuclear localization sequence located at amino acids 718-584, a
XX transactivator domain (N-TAD) located between amino acids 531 and 584,
XX and a second transactivator domain (C-TAD) located between 813 and 826.
XX The invention relates to isolated variants of HIF-1alpha, such as that
XX represented by the present sequence. The variants are useful for
XX identifying compounds capable of modulating the function of a functional
XX domain of human HIF-1alpha. The method comprises contacting a candidate
XX compound with a cell expressing a HIF-1alpha variant conjugated to a
XX molecular probe. The localization of the probe can be detected in the
XX cell. The Aequorea victoria green fluorescent protein can be used as the
XX molecular probe. The compounds are useful for the regulation of HIF-
XX 1alpha target genes, such as those involved in the regulation of
XX angiogenesis, erythropoiesis and glycolysis
XX Sequence 311 AA;
SQ Query Match 100.0%; Score 101; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 8.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFOL 19
DB 226 DLDLEMLAPYIPMDDDFOL 244
RESULT 27
ADO39389
ID ADO39389 standard; protein; 409 AA.
XX AC ADO39389;
XX 15-JUL-2004 (first entry)
XX Chimeric transactivator THV fragment #3.
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
XX normoxia; transcription factor degradation; anaemia; AIDS; cancer;
XX inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
XX tetracycline resistance; VP16.
XX OS Homo sapiens.
XX PN US2004018606-A1.
XX PD 29-JAN-2004.
XX PF 30-APR-2003; 2003US-00425833.
XX PR 30-APR-2002; 2002US-0376269P.
XX PA (BOHL/) BOHL D.
XX (HEAR/) HEAR M.
XX PI Bohl D, Heard M;
XX WPI; 2004-122040/12.
XX N-PSDB; ADO39384.
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
XX of a transcription factor susceptible to degradation under normoxia
XX conditions, useful for treating anemia associated with AIDS, cancer and
XX inflammation.
XX Disclosure; Fig 6H; 28pp; English.
XX The invention describes an isolated polynucleotide (I) which codes for a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions. Also described are: a chimeric transactivator comprising a
XX domain of a transcription factor wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions; an isolated polynucleotide which codes for the chimeric
XX transactivator (1); a vector comprising the chimeric transactivator
XX polynucleotide (2); a composition comprising the chimeric transactivator
XX polynucleotide which contains a sequence that codes for a target gene and
XX a promoter which is regulated by the chimeric transactivator coded; a
XX method of expressing a target gene in a subject, comprising administering
XX the composition of (4); a method of increasing the number of red blood
XX cells in a subject, comprising administering the composition of (4) to
XX the subject; and a method of increasing the number of blood vessels in
XX the subject, comprising administering the composition of (4) to the subject.
XX The methods and compositions of the present invention are useful for
XX treating anaemia associated with AIDS or cancer, anaemia from
XX inflammatory origin and haemoglobinopathies. This is the amino acid
XX sequence of a fragment of a chimeric transactivator comprising regions of
XX the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
XX transcription factor gene and VP16.
XX Sequence 409 AA;
SQ Query Match 100.0%; Score 101; DB 8; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFOL 19
DB 235 DLDLEMLAPYIPMDDDFOL 253
RESULT 28
AAB68415
ID AAB68415 standard; protein; 444 AA.
XX AC AAB68415;
```

AC AAB68415;
 XX 23-JUL-2001 (first entry)
 DE Amino acid sequence of tTAK-hH104.
 XX
 XX Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
 KW anemia; cancer; ischemia; erythropoietin; immunotherapy;
 KW autoimmune disease; hH104; tTAK.
 XX
 XX Synthetic.
 OS
 XX WO200136616-A2.
 XX
 XX 25-MAY-2001.
 XX
 XX 17-NOV-2000; 2000WO-FR003207.
 XX
 XX 18-NOV-1999; 99FR-00014513.
 XX
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX (AVET) AVENTIS PHARMA SA.
 XX
 XX Beuzard Y, Payen E, Scherman D, Bettan M;
 XX
 XX WPI; 2001-343818/36.
 XX
 XX N-PSDB; AAF85323.
 XX
 XX New nucleic acid construct for controlling expression of target gene,
 PT useful e.g. for treating cancer, is modulated by exogenous
 PT pharmaceutical and oxygen partial pressure.
 XX
 XX Disclosure; Page 57-58; 60pp; French.
 XX
 XX The specification describes a nucleic acid construct bearing a system for
 CC regulating the expression of a gene. The nucleic acid construct comprises
 CC at least one sequence encoding a protein that regulates expression of at
 CC least one gene of interest. The activity of this protein is modulated by
 CC presence/absence of a pharmacological agent and the amount of protein
 CC produced depends on the oxygen partial pressure. The constructs are used
 CC to treat conditions associated with cellular hypoxia, especially anemia,
 CC cancer and ischemia, specifically where the gene of interest encodes
 CC erythropoietin (but many other suitable genes are listed, e.g. those
 CC encoding single-chain antibodies for immunotherapy of infections or
 CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
 CC etc.). The present sequence is encoded by the open reading frame of tTAK-
 CC hH104. The sequence contains a human hH104 fragment, inserted into the
 CC BsiWI site of tTAK. The sequence is used to produce constructs of the
 CC invention
 XX
 XX Sequence 444 AA;
 SQ
 Query Match 100.0%; Score 101; DB 4; Length 444;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 242 DLDLEMLAPYIPMDDDFQL 260
 RESULT 29
 ADO39390
 ID ADO39390 standard; protein; 466 AA.
 XX
 XX ADO39390;
 AC
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX Chimeric transactivator THV fragment #4.
 DE
 XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.
 OS Homo sapiens.
 XX
 XX US2004018606-A1.
 XX
 XX 29-JAN-2004.
 XX
 XX 30-APR-2003; 2003US-00425833.
 XX
 XX 30-APR-2002; 2002US-0376269P.
 XX
 XX (BOHL/) BOHL D.
 XX (HEAR/) HEARD M.
 PA
 XX Bohl D, Heard M;
 PI
 XX
 XX WPI; 2004-122040/12.
 DR
 XX N-PSDB; ADO39385.
 DR
 XX
 XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
 PT of a transcription factor susceptible to degradation under normoxia
 PT conditions, useful for treating anemia associated with AIDS, cancer and
 PT inflammation.
 XX
 XX Disclosure; Fig 6I; 28pp; English.
 PS
 XX
 XX The invention describes an isolated polynucleotide (I) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions; an isolated polynucleotide which codes for the chimeric
 CC transactivator (1); a vector comprising the chimeric transactivator
 CC polynucleotide (2); a composition comprising polynucleotide (2) and a
 CC polynucleotide which contains a sequence that codes for a target gene and
 CC a promoter which is regulated by the chimeric transactivator coded; a
 CC method of expressing a target gene in a subject, comprising administering
 CC the composition of (4); a method of increasing the number of red blood
 CC cells in a subject, comprising administering the composition of (4) to
 CC the subject; and a method of increasing the number of blood vessels in
 CC subject, comprising administering the composition of (4) to the subject.
 CC The methods and compositions of the present invention are useful for
 CC treating anaemia associated with AIDS or cancer; anaemia from
 CC inflammatory origin and haemoglobinopathies. This is the amino acid
 CC sequence of a fragment of a chimeric transactivator comprising regions of
 CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
 CC transcription factor gene and VP16.
 XX
 XX Sequence 466 AA;
 SQ
 Query Match 100.0%; Score 101; DB 8; Length 466;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 235 DLDLEMLAPYIPMDDDFQL 253
 RESULT 30
 ADO39387
 ID ADO39387 standard; protein; 538 AA.
 XX
 XX ADO39387;
 AC
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX Chimeric transactivator THV fragment #1.
 DE
 XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
 KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
 KW

KW normoxia, transcription factor degradation; anaemia; AIDS; cancer;
 KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
 KW tetracycline resistance; VP16.

OS Homo sapiens.

PN US2004018606-A1.

XX 29-JAN-2004.

XX 30-APR-2003; 2003US-00425833.

XX 30-APR-2002; 2002US-0376269P.

XX (BOHL/) BOHL D.
 XX (HEAR/) HEARD M.

XX Bohl D, Heard M;

XX WPI; 2004-122040/12.

XX N-PSDB; ADO39382.

XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
 PT of a transcription factor susceptible to degradation under normoxia
 PT conditions, useful for treating anemia associated with AIDS, cancer and
 PT inflammation.

PS Disclosure; Fig 6F; 28pp; English.

XX The invention describes an isolated polynucleotide (I) which codes for a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions. Also described are: a chimeric transactivator comprising a
 CC domain of a transcription factor, wherein the domain confers to the
 CC transcription factor susceptibility to degradation under normoxia
 CC conditions; an isolated polynucleotide which codes for the chimeric
 CC transactivator (1); a vector comprising the chimeric transactivator
 CC polynucleotide (2); a composition comprising polynucleotide (2) and a
 CC polynucleotide which contains a sequence that codes for a target gene and
 CC a promoter which is regulated by the chimeric transactivator coded; a
 CC method of expressing a target gene in a subject, comprising administering
 CC the composition of (4); a method of increasing the number of red blood
 CC cells in a subject, comprising administering the composition of (4) to
 CC the subject; and a method of increasing the number of blood vessels in
 CC a subject, comprising administering the composition of (4) to the subject.
 CC The methods and compositions of the present invention are useful for
 CC treating anaemia associated with AIDS or cancer, anaemia from
 CC inflammatory origin and haemoglobinopathies. This is the amino acid
 CC sequence of a fragment of a chimeric transactivator comprising regions of
 CC the tetracycline resistance gene, mouse hypoxia-induced factor 1.(HIF-1)
 CC transcription factor gene and VP16.

XX Sequence 538 AA;

Query Match 100.0%; Score 101; DB 8; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
 DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 31

ID ABP41474 standard; protein; 542 AA.

XX ABP41474;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HNORJ10, SEQ ID NO:2606.

XX

KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 14q21-24.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ54551.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 2606; 2922pp; English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 542 AA;

Query Match 100.0%; Score 101; DB 5; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
 |||||

```
Db 272 DLDLEMLAPYIPMDDDFQL 290
RESULT 32
ADO39388
ID ADO39388 standard; protein; 595 AA.
AC ADO39388;
XX
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #2.
XX
XX haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
XX Homo sapiens.
XX
XX US2004018606-A1.
XX
XX 29-JAN-2004.
XX
XX 30-APR-2003; 2003US-00425833.
XX
XX 30-APR-2002; 2002US-0376269P.
XX
XX (BOHL/) BOHL D.
XX (HEAR/) HEARD M.
XX
XX Bohl D, Heard M;
XX
XX WPI: 2004-122040/12.
XX N-PSDB; ADO39383.
XX
XX New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
XX of a transcription factor susceptible to degradation under normoxia
XX conditions, useful for treating anemia associated with AIDS, cancer and
XX inflammation.
XX
XX Disclosure; Fig 6G; 28pp; English.
XX
XX The invention describes an isolated polynucleotide (1) which codes for a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions. Also described are: a chimeric transactivator comprising a
XX domain of a transcription factor, wherein the domain confers to the
XX transcription factor susceptibility to degradation under normoxia
XX conditions; an isolated polynucleotide which codes for the chimeric
XX transactivator (1); a vector comprising the chimeric transactivator
XX polynucleotide (2); a composition comprising polynucleotide (2) and a
XX polynucleotide which contains a sequence that codes for a target gene and
XX a promoter which is regulated by the chimeric transactivator coded; a
XX method of expressing a target gene in a subject, comprising administering
XX the composition of (4); a method of increasing the number of red blood
XX cells in a subject, comprising administering the composition of (4) to
XX the subject; and a method of increasing the number of blood vessels in
XX a subject, comprising administering the composition of (4) to the subject.
XX The methods and compositions of the present invention are useful for
XX treating anaemia associated with AIDS or cancer, anaemia from
XX inflammatory origin and haemoglobinopathies. This is the amino acid
XX sequence of a fragment of a chimeric transactivator comprising regions of
XX the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
XX transcription factor gene and VP16.
XX
XX Sequence 595 AA;
XX
XX Query Match 100.0%; Score 101; DB 8; Length 595;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDLEMLAPYIPMDDDFQL 19
Db 343 DLDLEMLAPYIPMDDDFQL 361
RESULT 34
AAU77614
ID AAU77614 standard; protein; 613 AA.
Db 364 DLDLEMLAPYIPMDDDFQL 382
RESULT 33
AAU94630
ID AAU94630 standard; protein; 613 AA.
AC AAU94630;
XX
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/delta178-390.
XX
XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
XX Homo sapiens.
XX
XX WO2000029437-A1.
XX
XX 25-MAY-2000.
XX
XX 11-NOV-1999; 99WO-SE002053.
XX
XX 13-NOV-1998; 98SE-00003891.
XX
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX Berkenstam A, Poellinger L;
XX
XX WPI; 2000-399715/34.
XX
XX Human hypoxia-inducible factor alpha variants for identifying compounds
XX that modulate its functional domain and regulate genes involved in
XX angiogenesis, erythropoiesis.
XX
XX Claim 13; Page 72-74; 87pp; English.
XX
XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
XX -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
XX multi-step process which includes hypoxia-dependent nuclear import and
XX activation of the transactivation domain. The HIF-1alpha consists of a
XX number of functional domains including a PAS-B (Per, Arnt, Sim) domain
XX located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
XX nuclear localization sequence located at amino acids 718-584, a
XX transactivator domain (N-TAD) located between amino acids 531 and 584,
XX and a second transactivator domain (C-TAD) located between 813 and 826.
XX The invention relates to isolated variants of HIF-1alpha, such as that
XX represented by the present sequence. The variants are useful for
XX identifying compounds capable of modulating the function of a functional
XX domain of human HIF-1alpha. The method comprises contacting a candidate
XX compound with a cell expressing a HIF-1alpha variant conjugated to a
XX molecular probe. The localization of the probe can be detected in the
XX cell. The Aequorea victoria green fluorescent protein can be used as the
XX molecular probe. The compounds are useful for the regulation of HIF-
XX 1alpha target genes, such as those involved in the regulation of HIF-
XX angiogenesis, erythropoiesis and glycolysis
XX
XX Sequence 613 AA;
XX
XX Query Match 100.0%; Score 101; DB 3; Length 613;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDLEMLAPYIPMDDDFQL 19
Db 343 DLDLEMLAPYIPMDDDFQL 361
RESULT 34
AAU77614
ID AAU77614 standard; protein; 613 AA.
```

XX AAU77614;
XX 05-JUN-2002 (first entry)
XX Human hypoxia-inducible factor-1 alpha, HIF-1, mutant delta 178-390.
XX Human; HIF-1; hypoxia-inducible factor-1; rheumatoid arthritis;
KW transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction;
KW circulatory disorder; cancer; hypertension; demyelinating disorder;
KW angiogenesis; sarcoidosis; hepatitis-caused inflammation;
KW chronic ulceration; neovascularisation; arterial hypervascularisation;
KW bullous skin disease; vasculitis; dermatomyositis; polymyositis; mutant;
KW mutin; Y565G.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 177..178
FT /note= "Residues 178-390 of the wild-type HIF-1 have been
FT deleted"
FT
XX
XX WO200212326-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-IB001775.
XX
XX 07-AUG-2000; 2000US-0223480P.
XX
XX (ASPE-) ASPERA PHARM AB.
XX
XX Poellinger L, Pereira T, Ruas J;
XX
XX WPI; 2002-257466/30.
XX
XX New polypeptides comprising hypoxia-inducible factor-1 with alterations
PT of the transactivation domain, useful treating ischemic conditions, e.g.
PT brain infarction, heart infarction or circulatory disorder.
XX
XX Example 5; Page; 80pp; English.
XX
XX The invention relates to a polypeptide comprising hypoxia-inducible
CC factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or
CC C-TAD). Also included are nucleic acids encoding the altered proteins, a
CC vector comprising the nucleic acid, a host cell transformed with the
CC vector, methods for producing the protein or its functional fragment or
CC an isolated degradation box, a method of screening for an agent that
CC modulates N-TAD function and antagonists, agonists, modulators and HIF-1
CC peptide fragments useful for modulating HIF-1 function or the function of
CC proteins that interact with it. The isolated polypeptides and their
CC fragments with altered residues are useful in methods for treating
CC diseases. The disease is an ischaemic condition, e.g. brain infarction,
CC heart infarction or circulatory disorder. The disease may also be cancer,
CC hypertension, demyelinating disorders, diffuse proliferative
CC glomerulonephritis, toxoplasmosis caused retinohorioiditis, HIV (human
CC immunodeficiency virus) caused Tat angiogenesis, HIV-caused Kaposi's
CC sarcoma, hepatitis-caused inflammation, hepatitis-caused angiogenesis,
CC chronic ulceration, proliferative retinopathy, retina haemangioblastomas,
CC neovascularisation, arterial hypervascularisation, sarcoidosis, bullous
CC skin disease, vasculitis with angiogenesis, dermatomyositis with
CC angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis,
CC juvenile osteoarthritis, polyarthritis, aneurysm or atheroma. The present
CC sequence represents HIF-1 mutant delta 178-390. Note: The present
CC sequence is not shown in the specification but was created by the indexer
CC using the information in example 5 and the HIF sequence appearing as
CC AAU77602
XX
XX Sequence 613 AA;

Query Match 100.0%; Score 101; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFOL 19
|||||
DB 343 DLDLEMLAPYIPMDDDFOL 361
RESULT 35
ADO39391
ID ADO39391 standard; protein; 632 AA.
XX
AC ADO39391;
XX
DT 15-JUL-2004 (first entry)
XX
XX Chimeric transactivator THV fragment #5.
XX
DE
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-induced factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
FN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEAR M.
PI Bohl D, Heard M;
XX
XX WPI; 2004-122040/12.
DR N-PSDB; ADO39386.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
XX inflammation.
PS Disclosure; Fig 6J; 28pp; English.
XX
XX The invention describes an isolated polynucleotide (1) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC the subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
XX Sequence 632 AA;

Query Match 100.0%; Score 101; DB 8; Length 632;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
|||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 36

AA94629
ID AAY94629 standard; protein; 652 AA.

XX AC AAY94629;

XX 15-AUG-2000 (first entry)

XX HIF-1alpha variant protein sequence HIF-1alpha/1-652.

XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Berkenstam A, Poellinger L;

XX WPI; 2000-399715/34.

PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.

PS Claim 15; Page 69-70; 87pp; English.

CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 531 and 584, a
CC transactivator domain (N-TAD) located between amino acids 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aqueora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of HIF-
CC angiogenesis, erythropoiesis and glycolysis

XX Sequence 652 AA;

Query Match 100.0%; Score 101; DB 3; Length 652;

Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

|||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 37

AA84167
ID AAY84167 standard; protein; 669 AA.

XX AC AAY84167;

XX 03-JUL-2000 (first entry)

XX A variant of human hypoxia inducible factor-1 alpha protein.

XX Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.

XX Synthetic.

OS Homo sapiens.

XX WO200010578-A1.

XX 02-MAR-2000.

XX 25-AUG-1999; 99WO-US019416.

XX 25-AUG-1998; 98US-00148547.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Semenza GL;

XX WPI; 2000-246493/21.

XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX treating hypoxia or ischemia-related tissue damage.

XX Claim 1; Page; 96pp; English.

XX The present sequence represents a variant of hypoxia-inducible factor
XX (HIF)-1 alpha, comprising amino acids 1-391 and 549-826 of the wild type
XX protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
XX and non-hypoxic conditions. The variants comprises amino acid residues 1-
XX 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
XX 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
XX which residues 551 and 552 are not serine and threonine, respectively.
XX The HIF-1alpha variant polynucleotide sequences are useful for increasing
XX expression of a hypoxia inducible gene in a cell. They are also useful for
XX providing constitutive expression of a hypoxia inducible factor in a
XX cell, and for reducing or preventing hypoxia or ischemia related damage.
XX The variant HIF-1alpha polypeptides are useful for providing prophylactic
XX therapy for inducing the level of angiogenesis in tissues of patients at
XX risk of coronary artery disease or ischemic tissue damage. Note: this
XX sequence does not appear in the specification; it was created using
XX information provided

XX Sequence 669 AA;

Query Match 100.0%; Score 101; DB 3; Length 669;

Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

|||
Db 399 DLDLEMLAPYIPMDDDFQL 417

RESULT 38

AA84166
ID AAY84166 standard; protein; 697 AA.

XX AC AAY84166;

XX 03-JUL-2000 (first entry)

XX DE A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 422 /note= "this residue is optionally not Ser, and is
FT preferably Gly"
FT Misc-difference 423 /note= "this residue is optionally not Thr, and is
FT preferably Ala"
XX
PN WO200010578-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019416.
XX
PR 25-AUG-1998; 98US-00148547.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Semenza GL;
XX
XX WPI; 2000-246493/21.
DR
PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.
XX
PS Claim 1; Page; 96pp; English.
XX
CC The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 521-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 576-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They are also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 697 AA;
Query Match 100.0%; Score 101; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 427 DLDLEMLAPYIPMDDDFQL 445
RESULT 39
AAY84173
ID AAY84173 standard; protein; 701 AA.
XX
AC AAY84173;
XX
DT 03-JUL-2000 (first entry)
DE A variant of human hypoxia inducible factor-1 alpha protein.

XX DE A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 426 /note= "this residue is not Ser, and is preferably Gly"
FT Misc-difference 427 /note= "this residue is not Thr, and is preferably Ala"
XX
PN WO200010578-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019416.
XX
PR 25-AUG-1998; 98US-00148547.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Semenza GL;
XX
XX WPI; 2000-246493/21.
DR
PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.
XX
PS Claim 1; Page; 96pp; English.
XX
CC The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 517-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They are also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 701 AA;
Query Match 100.0%; Score 101; DB 3; Length 701;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFQL 19
|||||
Db 431 DLDLEMLAPYIPMDDDFQL 449
RESULT 40
AAY84172
ID AAY84172 standard; protein; 710 AA.
XX
AC AAY84172;
XX
DT 03-JUL-2000 (first entry)
DE A variant of human hypoxia inducible factor-1 alpha protein.

```

XX Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX Synthetic.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Key
FT Misc-difference 435
FT /note= "this residue is not Ser, and is preferably Gly"
FT Misc-difference 436
FT /note= "this residue is not Thr, and is preferably Ala"
XX WO200010578-A1.
XX 02-MAR-2000.
XX 25-AUG-1999; 99WO-US019416.
XX 25-AUG-1998; 98US-00148547.
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX Semenza GL;
XX WPI; 2000-246493/21.
XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX treating hypoxia or ischemia-related tissue damage.
XX Claim 1; Page; 96pp; English.
XX The present sequence represents a variant of hypoxia-inducible factor
XX (HIF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild type
XX protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
XX and non-hypoxic conditions. The variants comprises amino acid residues 1-
XX 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
XX 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
XX which residues 551 and 552 are not serine and threonine, respectively.
XX The HIF-1alpha variant polynucleotide sequences are useful for increasing
XX expression of a hypoxia inducible gene in a cell. They are also useful for
XX providing constitutive expression of a hypoxia inducible factor in a
XX cell, and for reducing or preventing hypoxia or ischemia related damage.
XX The variant HIF-1alpha polypeptides are useful for providing prophylactic
XX therapy for inducing the level of angiogenesis in tissues of patients at
XX risk of coronary artery disease or ischemic tissue damage. note: this
XX sequence does not appear in the specification; it was created using
XX information provided
XX SQ Sequence 710 AA;
XX Query Match 100.0%; Score 101; DB 3; Length 710;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 DLDLEMLAPYIPMDDDFQL 19
XX 440 DLDLEMLAPYIPMDDDFQL 458
XX RESULT 41
XX AAY84171
XX ID AAY84171 standard; protein; 724 AA.
XX AC AAY84171;
XX 03-JUL-2000 (first entry)
XX DE A variant of human hypoxia inducible factor-1 alpha protein.
XX Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX Synthetic.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Key
FT Misc-difference 435
FT /note= "this residue is not Ser, and is preferably Gly"
FT Misc-difference 436
FT /note= "this residue is not Thr, and is preferably Ala"
XX WO200010578-A1.
XX 02-MAR-2000.
XX 25-AUG-1999; 99WO-US019416.
XX 25-AUG-1998; 98US-00148547.
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX Semenza GL;
XX WPI; 2000-246493/21.
XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX treating hypoxia or ischemia-related tissue damage.
XX Claim 1; Page; 96pp; English.
XX The present sequence represents a variant of hypoxia-inducible factor
XX (HIF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild type
XX protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
XX and non-hypoxic conditions. The variants comprises amino acid residues 1-
XX 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
XX 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
XX which residues 551 and 552 are not serine and threonine, respectively.
XX The HIF-1alpha variant polynucleotide sequences are useful for increasing
XX expression of a hypoxia inducible gene in a cell. They are also useful for
XX providing constitutive expression of a hypoxia inducible factor in a
XX cell, and for reducing or preventing hypoxia or ischemia related damage.
XX The variant HIF-1alpha polypeptides are useful for providing prophylactic
XX therapy for inducing the level of angiogenesis in tissues of patients at
XX risk of coronary artery disease or ischemic tissue damage. note: this
XX sequence does not appear in the specification; it was created using
XX information provided
XX SQ Sequence 724 AA;
XX Query Match 100.0%; Score 101; DB 3; Length 724;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 DLDLEMLAPYIPMDDDFQL 19
XX 454 DLDLEMLAPYIPMDDDFQL 472
XX RESULT 42
XX ABR82375
XX ID ABR82375 standard; protein; 735 AA.
XX AC ABR82375;
XX 06-NOV-2003 (first entry)
XX DE Hypoxia-inducible factor 1 (HIF-1) alpha variant sequence.
XX HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
XX erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquilizer; vulnerary; cardiant; cerebroprotective; variant.

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XX OS Homo sapiens.
XX XX
XX PN WO2003057820-A2.
XX XX
XX PD 17-JUL-2003.
XX PF
XX PF 04-OCT-2002; 2002WO-US031699.
XX PR
XX PR 21-DEC-2001; 2001US-00032361.
XX XX
XX PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
XX PI McGrath K;
XX XX
XX DR WPI; 2003-645988/61.
XX XX
XX PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
XX PT ubiquitination, and activator of vascular endothelial growth factor
XX PT transcription useful for treating tissue injuries including wounds,
XX PT surgical incisions.
XX XX
XX PS Disclosure; Page 5-6; 37pp; English.
XX XX
XX CC The invention relates to peptide inhibitors of hypoxia-inducible factor
XX CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
XX CC transcription of erythropoietin (EPO), vascular endothelial growth factor
XX CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
XX CC for treating tissue injuries including wounds, surgical incisions,
XX CC chronic wounds, heart disease and stroke. The present sequence represents
XX CC a HIF-1 alpha variant sequence
XX XX
XX SQ Sequence 735 AA;

Query Match 100.0%; Score 101; DB 6; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574
|||||
RESULT 43
ADN75066
ID ADN75066 standard; protein; 735 AA.
XX AC ADN75066;
XX XX
XX DT 12-AUG-2004 (first entry)
XX DE Human hypoxia-inducible factor 1 alpha #2.
XX XX
XX KW human; antisense therapy; hypoxia-inducible factor 1 alpha;
XX KW hyperproliferative disorder.
XX OS Homo sapiens.
XX XX
XX PN US2004101858-A1.
XX PD
XX PD 27-MAY-2004.
XX XX
XX PF 23-NOV-2002; 2002US-00304126.
XX XX
XX PR 23-NOV-2002; 2002US-00304126.
XX XX
XX -PA (ISIS-) ISIS PHARM INC.
XX PI Ward DT, Dobie KW;
XX XX
XX DR WPI; 2004-399686/37.
XX DR N-PSDB; ADN74945.
XX XX

PT New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding hypoxia-inducible factor 1 alpha, useful for treating diseases
PT associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative
PT disorders.
XX XX
XX PS Disclosure; Page 57-59; 80pp; English.
XX XX
XX CC The invention relates to antisense oligonucleotides targeted to, and
XX CC which specifically hybridize with, and inhibit expression of, a nucleic
XX CC acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense
XX CC oligonucleotides are useful for treating a disease or condition
XX CC associated with hypoxia-inducible factor 1 alpha, such as a
XX CC hyperproliferative disorder. They are also useful in research and
XX CC diagnostics for modulating the expression of hypoxia-inducible factor 1
XX CC alpha. The present sequence represents human hypoxia-inducible factor 1
XX CC alpha #2.
XX XX
XX SQ Sequence 735 AA;

Query Match 100.0%; Score 101; DB 8; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574
|||||
RESULT 44
AA84170
ID AA84170 standard; protein; 749 AA.
XX AC AA84170;
XX XX
XX DT 03-JUL-2000 (first entry)
XX DE A variant of human hypoxia inducible factor-1 alpha protein.
XX XX
XX KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
XX KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
XX KW ischemia related damage; angiogenesis; coronary artery disease;
XX KW ischemic tissue damage.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 474 /note= "this residue is not Ser, and is preferably Gly"
XX FT Misc-difference 475 /note= "this residue is not Thr, and is preferably Ala"
XX XX
XX PN WO200010578-A1.
XX XX
XX PD 02-MAR-2000.
XX XX
XX PF 25-AUG-1999; 99WO-US019416.
XX XX
XX PR 25-AUG-1998; 98US-00148547.
XX XX
XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PI Semenza GL;
XX XX
XX DR WPI; 2000-246493/21.
XX XX
XX PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
XX PT treating hypoxia or ischemia-related tissue damage.
XX XX
XX PS Claim 1; Page; 96pp; English.
XX XX
XX CC The present sequence represents a variant of hypoxia-inducible factor
XX CC (HIF)-1 alpha, comprising amino acids 1-391 and 469-826 of the wild type

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CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variant comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They are also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided

XX
SQ Sequence 749 AA;

Query Match 100.0%; Score 101; DB 3; Length 749;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 479 DLDLEMLAPYIPMDDDFQL 497
|||||

RESULT 45
AAY94635
ID AAY94635 standard; protein; 756 AA.

XX
AC AAY94635;

XX 15-AUG-2000 (first entry)

DE HIF-1alpha variant protein sequence HIF-1alpha/71-826.

XX Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.

XX Homo sapiens.

XX WO200029437-A1.

XX 25-MAY-2000.

XX 11-NOV-1999; 99WO-SE002053.

XX 13-NOV-1998; 98SE-00003891.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Berkenstam A, Poellinger L;

XX WPI; 2000-399715/34.

XX Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.

XX Claim 20; Page 79-82; 87pp; English.

XX This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transcription domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional

CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequorea victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis

XX Sequence 756 AA;

Query Match 100.0%; Score 101; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19
DB 486 DLDLEMLAPYIPMDDDFQL 504
|||||

RESULT 46
AAY84169

XX AAY84169 standard; protein; 789 AA.

XX AAY84169;

XX 03-JUL-2000 (first entry)

DE A variant of human hypoxia inducible factor-1 alpha protein.

XX Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 514

XX /note= "this residue is not Ser, and is preferably Gly"

XX Misc-difference 515

XX /note= "this residue is not Thr, and is preferably Ala"

XX WO200010578-A1.

XX 02-MAR-2000.

XX 25-AUG-1999; 99WO-US019416.

XX 25-AUG-1998; 98US-00148547.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Semenza GL;

XX WPI; 2000-246493/21.

XX Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.

XX Claim 1; Page; 96pp; English.

XX The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 429-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They are also useful for
CC providing constitutive expression of a hypoxia inducible factor in a

CC cell, and for reducing or preventing hypoxia or ischemia related damage.
 CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
 CC therapy for inducing the level of angiogenesis in tissues of patients at
 CC risk of coronary artery disease or ischemic tissue damage. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 789 AA;

SQ Query Match 100.0%; Score 101; DB 3; Length 789;

Best Local Similarity 100.0%; Pred. No. 2.4e-07; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

DB 519 DLDLEMLAPYIPMDDDFQL 537

RESULT 47

ADA18535
 ID ADA18535 standard; protein; 789 AA.

XX AC ADA18535;

XX DT 20-NOV-2003 (first entry)

XX DE Human hypoxia inducible factor-1, HIF-1alpha, mutant SHIF-1alpha #3.

XX KW hypoxia inducible factor-1; HIF-1alpha; human; vasotropic; gene therapy;
 XX KW hypoxia; ischaemia-related tissue damage; erythropoiesis; anaemia;
 XX KW altitude sickness; neovascularisation; ischaemic myocardium; mutant;
 XX KW murein.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 391..392
 FT /note= "Amino acids 392-428 of the wild-type protein have
 FT been deleted"

FT Misc-difference 514

FT /label= UNKNOWN

FT /note= "Wild-type Ser substituted by Xaa (any amino
 FT acid)"

FT Misc-difference 515
 FT /note= "Wild-type Thr substituted by Ala"

XX US6562799-B1.

XX PD 13-MAY-2003.

XX PF 25-AUG-1999; 99US-00383581.

XX PR 25-AUG-1998; 98US-00148547.

XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Semenza GL;

XX WPI; 2003-605425/57.

XX New human hypoxia-inducible factor-1alpha proteins and nucleic acids,
 PT useful for treating or preventing hypoxia- or ischemia-related tissue
 PT damage.

XX Claim 21; Page; 32pp; English.

XX The invention relates to a new isolated nucleic acid molecule encoding a
 CC human hypoxia-inducible factor-1alpha (HIF-1alpha) comprising amino acid
 CC residues: 1-391 and 521-826; 1-391 and 549-826; 1-391 and 576-826; or 1-
 CC 391 and 429-826, of ADA18531, where amino acid residues 551 and 552 are
 CC no longer serine and threonine. Also included are an expression vector
 CC comprising HIF-1 alpha, increasing expression of a hypoxia inducible gene

CC in a cell, increasing expression of a hypoxia inducible gene in a cell,
 CC reducing hypoxia or ischaemia-related tissue damage in a subject by
 CC administering HIF-1alpha at a site of hypoxia or ischaemia-related tissue
 CC damage, an isolated nucleic acid molecule comprising a polynucleotide
 CC encoding a stable form of human hypoxia-inducible factor-1alpha (SHIF-
 CC 1alpha) having the sequence of ADA18531 except that amino acid residues
 CC 392-428 are deleted, and amino acid residues 551 and 552 are changed from
 CC serine and threonine to any other amino acid respectively, an expression
 CC vector comprising the nucleic acid, an isolated host cell containing the
 CC vector, inducing angiogenesis in a mammalian tissue and a formulation for
 CC administration of a polynucleotide encoding SHIF-1alpha to a patient
 CC having hypoxia-related tissue damage The HIF-1alpha is useful for
 CC treating or preventing hypoxia- or ischaemia-related tissue damage e.g.
 CC erythropoiesis in anaemia, altitude sickness and neovascularisation in
 CC ischaemic myocardium. The HIF-1alpha polypeptides may also be used to
 CC produce antibodies which are immunoreactive or selectively bind to
 CC epitopes of SHIF-1alpha polypeptides. The present sequence represents the
 CC SHIF-1 alpha mutant where acid residues 551 and 552 are mutated and amino
 CC acids 392-428 are deleted. Note: The present sequence is not shown in the
 CC specification but was created by the indexer using the wild-type HIF-1
 CC sequence and the information in the claims

XX SQ Sequence 789 AA;

Query Match 100.0%; Score 101; DB 6; Length 789;

Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

DB 519 DLDLEMLAPYIPMDDDFQL 537

RESULT 48

ADA18533
 ID ADA18533 standard; protein; 789 AA.

XX AC ADA18533;

XX DT 20-NOV-2003 (first entry)

XX DE Human hypoxia inducible factor-1, HIF-1alpha, mutant SHIF-1alpha.

XX KW hypoxia inducible factor-1; HIF-1alpha; human; vasotropic; gene therapy;
 KW hypoxia; ischaemia-related tissue damage; erythropoiesis; anaemia;
 KW altitude sickness; neovascularisation; ischaemic myocardium; mutant;
 KW murein.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 391..392
 FT /note= "Amino acids 392-428 of the wild-type protein have
 FT been deleted"

FT Misc-difference 514..515

FT /label= UNKNOWN

FT /note= "Wild-type Ser-Thr substituted by Xaa-Xaa (any
 FT amino acid)"

XX US6562799-B1.

XX PD 13-MAY-2003.

XX PF 25-AUG-1999; 99US-00383581.

XX PR 25-AUG-1998; 98US-00148547.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Semenza GL;

XX WPI; 2003-605425/57.

XX New human hypoxia-inducible factor-1alpha proteins and nucleic acids,
PT useful for treating or preventing hypoxia- or ischemia-related tissue
PT damage.
XX
XX
XX Claim 19; Page; 32pp; English.
XX
XX The invention relates to a new isolated nucleic acid molecule encoding a
CC human hypoxia-inducible factor-1alpha (HIF-1alpha) comprising amino acid
CC residues: 1-391 and 521-826; 1-391 and 549-826; 1-391 and 576-826; or 1-
CC 391 and 429-826, of ADA18531, where amino acid residues 551 and 552 are
CC no longer serine and threonine. Also included are an expression vector
CC comprising HIF-1 alpha, increasing expression of a hypoxia inducible gene
CC in a cell, increasing expression of a hypoxia inducible gene in a cell,
CC reducing hypoxia or ischaemia-related tissue damage in a subject by
CC administering HIF-1alpha at a site of hypoxia or ischaemia-related tissue
CC damage, an isolated nucleic acid molecule comprising a polynucleotide
CC encoding a stable form of human hypoxia-inducible factor-1alpha (shIF-
CC 1alpha) having the sequence of ADA18531 except that amino acid residues
CC 392-428 are deleted, and amino acid residues 551 and 552 are changed from
CC serine and threonine to any other amino acid respectively, an expression
CC vector comprising the nucleic acid, an isolated host cell containing the
CC vector, inducing angiogenesis in a mammalian tissue and a formulation for
CC administration of a polynucleotide encoding shIF-1alpha to a patient
CC having hypoxia-related tissue damage. The HIF-1alpha is useful for
CC treating or preventing hypoxia- or ischaemia-related tissue damage e.g.
CC erythropoiesis in anaemia, altitude sickness and neovascularisation in
CC ischaemic myocardium. The HIF-1alpha polypeptides may also be used to
CC produce antibodies which are immunoreactive or selectively bind to
CC epitopes of shIF-1alpha polypeptides. The present sequence represents the
CC shIF-1 alpha mutant where acid residues 551 and 552 are any amino acid
CC and amino acids 392-428 are deleted. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the wild-
CC type HIF-1 sequence and the information in the claims
XX
XX Sequence 789 AA;
XX
XX Query Match 100.0%; Score 101; DB 6; Length 789;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDLEMLAPYIPMDDDFQL 19
XX |||||
XX Db 519 DLDLEMLAPYIPMDDDFQL 537
XX
XX RESULT 49
XX ADA18534
XX ID ADA18534 standard; protein; 789 AA.
XX AC
XX AC ADA18534;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human hypoxia inducible factor-1, HIF-1alpha, mutant shIF-1alpha #2.
XX
XX KW hypoxia inducible factor-1; HIF-1alpha; human; vasotropic; gene therapy;
XX KW hypoxia; ischaemia-related tissue damage; erythropoiesis; anaemia;
XX KW altitude sickness; neovascularisation; ischaemic myocardium; mutant;
XX KW mutin.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 391..392
XX FT /note= "Amino acids 392-428 of the wild-type protein have
XX FT been deleted"
XX FT Misc-difference 514
XX FT /note= "Wild-type Ser substituted by Gly"
XX FT Misc-difference 515
XX FT /label= UNKNOWN
XX FT /note= "Wild-type Thr substituted by Xaa (any amino
XX FT

FT acid)"
XX US562799-B1.
XX PD 13-MAY-2003.
XX PF 25-AUG-1999; 99US-00383581.
XX PR 25-AUG-1998; 98US-00148547.
XX PA (UYJ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PI Semenza GU;
XX DR WPI, 2003-605425/57.
XX
XX New human hypoxia-inducible factor-1alpha proteins and nucleic acids,
PT useful for treating or preventing hypoxia- or ischemia-related tissue
PT damage.
XX
XX Claim 20; Page; 32pp; English.
XX
XX The invention relates to a new isolated nucleic acid molecule encoding a
CC human hypoxia-inducible factor-1alpha (HIF-1alpha) comprising amino acid
CC residues: 1-391 and 521-826; 1-391 and 549-826; 1-391 and 576-826; or 1-
CC 391 and 429-826, of ADA18531, where amino acid residues 551 and 552 are
CC no longer serine and threonine. Also included are an expression vector
CC comprising HIF-1 alpha, increasing expression of a hypoxia inducible gene
CC in a cell, increasing expression of a hypoxia inducible gene in a cell,
CC reducing hypoxia or ischaemia-related tissue damage in a subject by
CC administering HIF-1alpha at a site of hypoxia or ischaemia-related tissue
CC damage, an isolated nucleic acid molecule comprising a polynucleotide
CC encoding a stable form of human hypoxia-inducible factor-1alpha (shIF-
CC 1alpha) having the sequence of ADA18531 except that amino acid residues
CC 392-428 are deleted, and amino acid residues 551 and 552 are changed from
CC serine and threonine to any other amino acid respectively, an expression
CC vector comprising the nucleic acid, an isolated host cell containing the
CC vector, inducing angiogenesis in a mammalian tissue and a formulation for
CC administration of a polynucleotide encoding shIF-1alpha to a patient
CC having hypoxia-related tissue damage. The HIF-1alpha is useful for
CC treating or preventing hypoxia- or ischaemia-related tissue damage e.g.
CC erythropoiesis in anaemia, altitude sickness and neovascularisation in
CC ischaemic myocardium. The HIF-1alpha polypeptides may also be used to
CC produce antibodies which are immunoreactive or selectively bind to
CC epitopes of shIF-1alpha polypeptides. The present sequence represents the
CC shIF-1 alpha mutant where acid residues 551 and 552 are mutated and amino
CC acids 392-428 are deleted. Note: The present sequence is not shown in the
CC specification but was created by the indexer using the wild-type HIF-1
CC sequence and the information in the claims
XX
XX SQ Sequence 789 AA;
XX
XX Query Match 100.0%; Score 101; DB 6; Length 789;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDLEMLAPYIPMDDDFQL 19
XX |||||
XX Db 519 DLDLEMLAPYIPMDDDFQL 537
XX
XX RESULT 50
XX AAW06558
XX ID AAW06558 standard; protein; 805 AA.
XX AC AAW06558;
XX AC
XX DT 19-MAR-1997 (first entry)
XX
XX DE Hypoxia inducible factor-1 alpha variant HIF-1 alpha delta-NB.
XX KW Hypoxia inducible factor-1 alpha; HIF-1; tissue damage; atherosclerosis;
XX KW cerebral artery disease; therapy.

XX Synthetic.
OS WO9639426-A1.
XX PD 12-DEC-1996.
XX PF 06-JUN-1996; 96WO-US010251.
XX PR 06-JUN-1995; 95US-00480473.
XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX PI Semenza GL;
XX WI; 1997-043061/04.
XX DNA encoding human hypoxia-inducible factor 1 alpha - useful for
PT enhancing expression of structural gene and treatment of hypoxia-related
PT tissue damage.
XX Claim 18; Page 58-60; 95pp; English.
XX Specific dominant-negative variant forms, HIF-1 alpha delta-NB (AAW06558)
CC and HIF-1 alpha delta-NB delta-AB (AAW06559), of human hypoxia-inducible
CC factor-1 (HIF-1) alpha subunit (see also AAW06557) both have the DNA-
CC binding domain of the native protein deleted, and the latter variant also
CC has a C-terminal truncation to improve stability in vivo. They can be
CC produced by the genetic engineering of HIF-1 alpha nucleic acids. The
CC variants dimerise with HIF-1 beta subunits to form nonfunctional HIF-1
CC complexes. Administration of a variant provides a means for treating HIF-
CC 1-mediated disorders
XX SQ Sequence 805 AA;
Query Match 100.0%; Score 101; DB 2; Length 805;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDLEMLAPYIPMDDDFQL 19
Db 535 DLDLEMLAPYIPMDDDFQL 553
Search completed: February 9, 2005, 06:05:42
Job time : 108 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 11 Seconds
(without alignments)
166.193 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 101

Sequence: 1 DLDLEMLAPYIPMDDDFQL 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : PIR 79:*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	810	2 JC4837	hypoxia-inducible
2	101	100.0	811	2 JC7619	hypoxia-inducible
3	101	100.0	813	2 JCS809	hypoxia-inducible
4	101	100.0	826	2 I38972	hypoxia-inducible
5	87	86.1	667	2 JC7771	hypoxia-inducible
6	54	53.5	1505	2 JC4851	hypoxia-inducible
7	46	45.5	113	2 AE0629	hypoxia-inducible
8	46	45.5	840	2 S41218	cell invasion prot
9	46	45.5	1499	2 B59431	HIR1 protein - yea
10	46	45.5	1501	2 T42724	Rho GTPase activat
11	45	44.6	800	2 S29344	p190-B protein - m
12	44	43.6	220	1 B5AG58	protein kinase KIN
13	44	43.6	220	1 AI3248	virB5 protein prec
14	44	43.6	707	1 Q0BEJ5	component of type
15	44	43.6	1666	1 C3CP	phosphotransferase
16	43.5	43.1	151	2 AC0367	complement C3 prec
17	43	42.6	444	2 AE0646	conserved hypothet
18	43	42.6	876	2 S62152	hypothetical prote
19	43	42.6	962	1 SNECPI	SFB2 protein - yea
20	43	42.6	962	2 H85933	pitrilysin (EC 3.4
21	43	42.6	962	2 F91088	proteinase III (im
22	42	41.6	96	2 S15152	proteinase III (im
23	42	41.6	214	2 G69380	hypothetical prote
24	42	41.6	220	1 B6AG55	virB5 protein prec
25	42	41.6	416	2 H95920	probable membrane-
26	42	41.6	451	2 D96981	sugar ABC transpor
27	42	41.6	452	2 F96981	sugar-binding peri
28	42	41.6	474	2 H84210	hypothetical prote
29	42	41.6	630	2 F95191	endopeptidase O [i

30	42	41.6	630	2 B98058	endopeptidase O (E
31	42	41.6	700	2 S38361	calpain (EC 3.4.22
32	42	41.6	726	2 AC27602	complement C3 - ra
33	42	41.6	962	2 AC0865	protease III precu
34	42	41.6	1221	2 E83327	conserved hypothet
35	42	41.6	2599	2 F90608	ABC transporter pe
36	41.5	41.1	426	2 A39695	transforming prote
37	41.5	41.1	437	2 S15704	transforming prote
38	41.5	41.1	441	1 TVCHMC	transforming prote
39	41	40.6	137	2 G70090	hypothetical prote
40	41	40.6	178	1 TVRTBM	transforming prote
41	41	40.6	310	1 S37695	calcium-binding pr
42	41	40.6	331	2 B55552	trans-o-hydrobenzy
43	41	40.6	367	1 E64070	histidinol-phospha
44	41	40.6	500	2 G71633	ADP-ATP carrier pr
45	41	40.6	684	2 G84730	Mutator-like trans
46	41	40.6	713	2 S76766	hypothetical prote
47	41	40.6	876	2 A89944	alanyl-tRNA synthet
48	41	40.6	887	2 S43196	(protein-Pil) urid
49	41	40.6	1471	2 D72758	hypothetical prote
50	40.5	40.1	415	2 B83634	hypothetical prote
51	40.5	40.1	474	2 F81283	hypothetical prote
52	40.5	40.1	507	2 I40767	catalase (EC 1.11.
53	40	39.6	256	2 F86856	catalase (EC 1.11.
54	40	39.6	334	2 H49343	hypothetical prote
55	40	39.6	354	2 AG3315	probable trans-o-h
56	40	39.6	360	2 G72673	lipopolysaccharide
57	40	39.6	374	2 T34435	hypothetical prote
58	40	39.6	390	2 F72863	AcOrf-109 protein
59	40	39.6	391	2 T41849	AcNPFV orf109 - Bo
60	40	39.6	422	2 G75131	malate oxidoreduct
61	40	39.6	439	2 H71072	probable malate de
62	40	39.6	471	2 T50016	transcription fact
63	40	39.6	550	2 T15868	hypothetical prote
64	40	39.6	593	2 H71283	conserved hypothet
65	40	39.6	660	2 S50383	gamma-glutamyltran

ALIGNMENTS

RESULT 1

JC4837

hypoxia-inducible factor 1 alpha - mouse

C:Species: Mus musculus (house mouse)

C>Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

C:Accession: JC4837

R:Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassemann, M.

Biochem. Biophys. Res. Commun. 223, 54-59, 1996

A>Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxi

A:Reference number: JC4837; MUID:96254028; PMID:8660378

A:Accession: JC4837

A:Molecule type: mRNA

A:Residues: 1-810 <WEN>

A:Cross-references: UNIPROT:Q61221; EMBL:X95580; NID:gi430864; PIDN:CAA64833.1; PID:gi437

C:Comment: This factor is involved in the oxygen-regulated transcription of several gene

C:Genetics:

A:Gene: Hif1alpha

A:Map position: 12

C:Keywords: transcription factor

F:5-58/Region: helix-loop-helix #status predicted

Query Match 100.0%; Score 101; DB 2; Length 810;

Best Local Similarity 100.0%; Pred. No. 3.5e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFQL 19

|||||

Db 543 DLDLEMLAPYIPMDDDFQL 561

RESULT 2

JC7619

hypoxia-inducible factor 1 alpha - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C:Accession: J07619
 R:Takahashi, T.; Sugishita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kinugawa, K.; Harada, Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001
 A>Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventricle
 A:Reference number: JC7619; MUID:21134360; PMID:11237772
 A:Contents: Embryonic ventricular myocytes
 A:Accession: JC7619
 A:Molecule type: mRNA
 A:Residues: 1-811 <TAK>
 A:Cross-references: DDBJ:AB013746
 A:Comment: This factor belongs to the basic helix-loop-helix-Per/ARNT/Sim (HLH-PAS) family of eukaryotic cells, and in redox stimuli.
 C:Genetics:
 A:Gene: hif-1alpha
 C:Keywords: embryo; transcription factor
 F:106-156/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS1>
 F:249-299/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS2>
 F:762-811/Domain: conserved carboxy-terminal transactivation element #status predicted <PAS3>
 F:767-768/Region: conserved dileucine repeat, important for oxygen-dependent degradation

Query Match 100.0%; Score 101; DB 2; Length 811;
 Best Local Similarity 100.0%; Pred. No. 3.5e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFOL 19
 |||||
 DB 554 DLDLEMLAPYIPMDDDFOL 572

RESULT 3
 JC5809
 hypoxia-inducible factor 1 alpha - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999
 C:Accession: JC5809
 R:Ladoux, A.; Frelin, C.
 Biochem. Biophys. Res. Commun. 240, 552-556, 1997
 A>Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop helix/PAS domain proteins in rat heart
 A:Reference number: JC5809; MUID:98063274; PMID:9398602
 A:Accession: JC5809
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-813 <LAD>
 C:Comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, and F16-144/Region: basic helix-loop-helix #status predicted

Query Match 100.0%; Score 101; DB 2; Length 813;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFOL 19
 |||||
 DB 543 DLDLEMLAPYIPMDDDFOL 561

RESULT 4
 I38972
 hypoxia-inducible factor 1 alpha - human
 N:Alternate names: ARNT interacting protein
 C:Species: Homo sapiens (man)
 C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C:Accession: I38972; G01875
 R:Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L. Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995
 A>Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulate transcription of a set of genes involved in cellular response to hypoxia
 A:Reference number: I38972; MUID:95296340; PMID:7539918
 A:Accession: I38972
 A>Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-826 <RES>
 A:Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g8813-3
 A>Note: parts of this sequence were confirmed by peptide sequencing
 R:Hoganesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: H00692
 A:Accession: G01875
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-826 <HOG>
 A:Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1; PID:g1144013
 C:Genetics:
 A:Gene: GDB:HIF1A
 A:Cross-references: GDB:512229
 A:Map position: 14q21-14q24
 C:Keywords: heterodimer

Query Match 100.0%; Score 101; DB 2; Length 826;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPMDDDFOL 19
 |||||
 DB 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 5
 JC7771
 hypoxia inducible factor-3 alpha - human
 C:Species: Homo sapiens (man)
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: JC7771
 R:Hara, S.; Hamada, J.; Kobayashi, C.; Kondo, Y.; Imura, N. Biochem. Biophys. Res. Commun. 287, 808-813, 2001
 A>Title: Expression and characterization of hypoxia-inducible factor (HIF)-3alpha in human cells
 A:Reference number: JC7771; PMID:11573933
 A:Contents: Kidney
 A:Accession: JC7771
 A:Molecule type: mRNA
 A:Residues: 1-667 <HAR>
 A:Cross-references: UNIPROT:Q9Y2N7; DDBJ:AB054067
 C:Comment: This protein is a heterodimeric transcription factor that belongs to the basic helix-loop-helix-PAS family of transcription factors involved in the regulation of hypoxia-inducible gene expression in human kidney.
 C:Genetics:
 A:Gene: hif-3alpha
 A:Map position: 19
 C:Keywords: kidney

Query Match 86.1%; Score 87; DB 2; Length 667;
 Best Local Similarity 94.4%; Pred. No. 5.2e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLEMLAPYIPMDDDFOL 19
 |||||
 DB 483 LDLEMLAPYISMDDDFOL 500

RESULT 6
 JC4851
 hypoxia-inducible factor 1 alpha homolog - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
 C:Accession: JC4851
 R:Nambu, J.R.; Chen, W.; Hu, S.; Crews, S.T. Gene 172, 249-254, 1996
 A>Title: The Drosophila melanogaster similar bHLH-PAS gene encodes a protein related to hypoxia-inducible factor 1
 A:Reference number: JC4851; MUID:96269413; PMID:8682312
 A:Accession: JC4851
 A:Molecule type: mRNA
 A:Residues: 1-1505 <NAM>
 A:Cross-references: UNIPROT:Q24167; GB:U43090; NID:g1174073; PIDN:AAC47303.1; PID:g11740
 C:Genetics:
 A:Gene: sima

A;Cross-references: FlyBase:FBgn0015542

A;Map position: 3

F;72-125/Region: helix-loop-helix #status predicted

F;171-433/Region: PAS domain #status predicted

F;506-635/Region: proline-rich

Query Match 53.5%; Score 54; DB 2; Length 1505;

Best Local Similarity 71.4%; Pred. No. 3.1;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 MLAPYIPMDDDFQL 19

|||||:|||||

DB 850 MKAPYIPIDDDMPL 863

RESULT 7

AS0629

cell invasion protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (st

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AE0629

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Conneron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AE0629

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-113 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD08216.1; PID:g16502264; GSPDB:GN00176

C;Genetics:

A;Gene: sigE

Query Match 45.5%; Score 46; DB 2; Length 113;

Best Local Similarity 50.0%; Pred. No. 2.8;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLEMLAPYIPMDDD 16

|||||:|||||

DB 37 DHTLEMLCCPFMLPDD 52

RESULT 8

S41218

HIR1 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YBL008w; protein YBL0318

C;Species: Saccharomyces cerevisiae

C;Date: 28-Jan-1994 #sequence_revision 09-Sep-1994 #text_change 16-Aug-2004

C;Accession: S41218; S45741; S33389; S38776

R;Delaveau, T.; Jacq, C.; Perea, J.

Yeast 8, 761-768, 1992

A;Title: Sequence of a 12.7 kb segment of yeast chromosome II identifies a PDR-like gene

A;Reference number: S25326; MUID:93070613; PMID:1441753

A;Accession: S41218

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-840

A;Cross-references: UNIPROT:P32479; EMBL:S47695; NID:g259049; PIDN:AAB23989.1; PID:g1680

A;Experimental source: strain S288C

R;Delaveau, T.; Jacq, C.; Perea, J.

submitted to the Protein Sequence Database, August 1994

A;Reference number: S45736

A;Accession: S45741

A;Molecule type: DNA

A;Residues: 1-840 <DE2>

A;Cross-references: EMBL:Z35769; NID:g535991; PIDN:CAA84827.1; PID:g535992; MIPS:YBL008w

A;Experimental source: strain S288C

R;Sherwood, P.W.; Tsang, S.V.M.; Osley, M.A.

Mol. Cell. Biol. 13, 28-38, 1993

A;Title: Characterization of HIR1 and HIR2, two genes required for regulation of histone

A;Reference number: S33389; MUID:93109312; PMID:8417331

A;Accession: S33389

A;Molecule type: DNA

A;Residues: 53-259, 'V', 261-339, 'M', 341-840 <SHE>

A;Cross-references: EMBL:L03838

R;Sherwood, P.W.; Tsang, S.V.; Osley, M.A.

submitted to the EMBL Data Library, October 1992

A;Reference number: S38776

A;Accession: S38776

A;Molecule type: DNA

A;Residues: 53-242, 'MGNILQFRTPLM', 255-259, 'V', 261-339, 'M', 341-840 <SH2>

A;Cross-references: EMBL:L03838

C;Genetics:

A;Gene: SGD:HIR1

A;Cross-references: SGD:S0000104; MIPS:YBL008w

A;Map position: 2L

C;Superfamily: WD repeat homology

C;Keywords: nucleus; transcription regulation

F;75-108/Domain: WD repeat homology <WD1>

F;133-166/Domain: WD repeat homology <WD2>

F;352-385/Domain: WD repeat homology <WD5>

Query Match 45.5%; Score 46; DB 2; Length 840;

Best Local Similarity 44.4%; Pred. No. 30;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LDLEMLAPYIPMDDDFQL 19

|||||:|||||

DB 53 MELESLTPELPDQLQM 70

RESULT 9

B59431

Rho GTPase activating protein 5 (p190-B) [imported] - human

C;Species: Homo sapiens (man)

C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C;Accession: B59431

R;Burbelo, P.D.; Miyamoto, S.; Utani, A.; Brill, S.; Yamada, K.M.; Hall, A.; Yamada, Y.

J. Biol. Chem. 270, 30919-30926, 1995

A;Title: p190-B, a new member of the Rho GAP family, and Rho are induced to cluster after

A;Reference number: B59431; MUID:96125066; PMID:8537347

A;Accession: B59431

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1499 <BUR>

A;Cross-references: UNIPROT:Q13017; GB:NP_001164; PID:g4502221; PIDN:NP_001164.1

Query Match 45.5%; Score 46; DB 2; Length 1499;

Best Local Similarity 52.6%; Pred. No. 61;

Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDLEMLAPYIPMDDDFQL 19

|||||:|||||

DB 982 DDDTEAPPPYSPIGDDVQL 1000

RESULT 10

T42724

p190-B protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T42724

R;Burbelo, P.D.; Finegold, A.A.; Kozak, C.A.; Yamada, Y.; Takami, H.

Biochim. Biophys. Acta 1443, 203-210, 1998

A;Title: Cloning, genomic organization and chromosomal assignment of the mouse p190-B gene

A;Reference number: Z22244; MUID:99057598; PMID:9838117

A;Accession: T42724

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1501 <BUR>

A;Cross-references: UNIPROT:P97393; EMBL:U67160; NID:g1762974; PID:g1762975; PIDN:AAD127

C;Genetics:

A;Map position: 12

Query Match 45.5%; Score 46; DB 2; Length 1501;
Best Local Similarity 52.6%; Pred. No. 61;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDFQL 19

||| ||| : |||

Db 981 DDDTEAPPYPSPIGDDVQL 999

RESULT 11

S29344 protein kinase KIN3 (EC 2.7.1.1-) - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein 05220; protein YOR233w

C;Species: *Saccharomyces cerevisiae*

C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Aug-2004

C;Accession: S29344; S67126; S24707

R;Kambouris, N.G.; Burke, D.J.; Creutz, C.E.

Yeast 9, 141-150, 1993

A;Title: Cloning and genetic analysis of the gene encoding a new protein kinase in *Sacch*

A;Reference number: S29344; MUID:93220392; PMID:8465601

A;Accession: S29344

A;Molecule type: DNA

A;Residues: 1-800 <KAM>

A;Cross-references: UNIPROT:Q01919; EMBL:X67916; NID:g5514; PIDN:CAA48115.1; PID:g5515

R;Boyer, J.; Fairhead, C.; Gallion, L.; Michaux, G.; Thierry, A.; Dujon, B

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67104

A;Accession: S67126

A;Molecule type: DNA

A;Residues: 1-800 <BOY>

A;Cross-references: EMBL:Z75141; NID:g1420534; PIDN:CAA99453.1; PID:e252094; PID:g142053

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:KIN4; KIN3; KIN31

A;Cross-references: SGD:S0005759; MIPS:YOR233w

A;Map position: 15R

C;Superfamily: protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F;44-313/Domain: protein kinase homology <KIN>

F;52-60/Region: protein kinase ATP-binding motif

Query Match 44.6%; Score 45; DB 2; Length 800;

Best Local Similarity 61.5%; Pred. No. 42;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MLAPYIPMDDDFQ 18

||| ||| : |||

Db 245 MLAGYLPWDDHHE 257

RESULT 12

BSAG58

virB5 protein precursor - *Agrobacterium tumefaciens* plasmid pTiC58

C;Species: *Agrobacterium tumefaciens*

C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004

C;Accession: S12345; S11830; S10520

R;Shirasu, K.; Morel, P.; Kado, C.I.

Mol. Microbiol. 4, 1153-1163, 1990

A;Title: Characterization of the virB operon of an *Agrobacterium tumefaciens* Ti plasmid:

A;Reference number: S12341; MUID:91041724; PMID:2233252

A;Accession: S12345

A;Molecule type: DNA

A;Residues: 1-220 <SHI>

A;Cross-references: UNIPROT:P17795; EMBL:J03320; NID:g154781; PIDN:AAA91595.1; PID:g1547

R;Rogowsky, P.M.; Powell, B.S.; Shirasu, K.; Lin, T.S.; Morel, P.; Zyprian, E.M.; Steck,

plasmid 23, 85-106, 1990

A;Title: Molecular characterization of the vir regulon of *Agrobacterium tumefaciens*: com

A;Residues: 1-220 <ROG>

A;Cross-references: EMBL:J03320; NID:g154781; PIDN:AAA91595.1; PID:g154787

R;Kulda, G.A.; de Vos, G.; Owen, J.; McCaffrey, G.; Zambryski, P.

Mol. Gen. Genet. 221, 256-266, 1990

A;Title: The virB operon of *Agrobacterium tumefaciens* pTiC58 encodes 11 open reading fra

A;Reference number: S10516; MUID:90318324; PMID:2370849

A;Accession: S10520

A;Molecule type: DNA

A;Residues: 1-220 <KUL>

A;Cross-references: EMBL:X53264; NID:g39152; PIDN:CAA37358.1; PID:g39157

C;Genetics:

A;Gene: virB5

A;Genome: plasmid

C;Superfamily: tumor-inducing plasmid pTiC58 virB5 protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-220/Product: virB5 protein #status predicted <MAT>

Query Match 43.6%; Score 44; DB 1; Length 220;

Best Local Similarity 61.5%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPM 13

||| ||| : |||

Db 81 DLDTEMFSPRMPM 93

RESULT 13

AI3248

component of type IV secretion system [imported] - *Agrobacterium tumefaciens* (strain C58

C;Species: *Agrobacterium tumefaciens*

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AI3248

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AI3248

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-220 <KUR>

A;Cross-references: UNIPROT:P17795; GB:AE008690; PIDN:AAL46407.1; PID:g17744201; GSPDB:G

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: virB5

A;Genome: plasmid

C;Superfamily: tumor-inducing plasmid pTiC58 virB5 protein

Query Match 43.6%; Score 44; DB 2; Length 220;

Best Local Similarity 61.5%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPM 13

||| ||| : |||

Db 81 DLDTEMFSPRMPM 93

RESULT 14

QOBEJ5

phosphotransferase (EC 2.7.1.1-) - human cytomegalovirus (strain AD169)

N;Alternate names: HSRF3 protein

C;Species: human cytomegalovirus, human herpesvirus 5

A;Note: host *Homo sapiens* (man)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: S09862

R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;

M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus

A;Reference number: S09749; MUID:90269039; PMID:2161319

Wed Feb 9 06:58:01 2005

Db 291 YVPLDDDYEV 300

RESULT 19

SNECPI

pitirylisin (EC 3.4.24.55) precursor [validated] - Escherichia coli (strain K-12)

N;Alternate names: endopeptidase Pi; proteinase III

C;Species: Escherichia coli

C;Date: 31-Mar-1993 #sequence revision 31-Oct-1997 #text_change 09-Jul-2004

C;Accession: F65064; A29093; A25765; B25532

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A67420; UID:97426617; PMID:9278503

A;Accession: F65064

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-962 <BLAT>

A;Cross-references: UNIPROT:P05458; GB:AE000365; GB:U00096; NID:g2367163; PIDN:AAC75860.

A;Experimental source: strain K-12, substrain MG1655

R;Claverie-Martin, F.; Diaz-Torres, M.R.; Kushner, S.R.

Gene 54, 185-195, 1987

A;Title: Analysis of the regulatory region of the protease III (ptr) gene of Escherichia

A;Reference number: A29093; UID:88005781; PMID:3308636

A;Accession: A29093

A;Molecule type: DNA

A;Residues: 1-276, 'HVHSLR', 283, 'W', 285-296 <CLA>

A;Cross-references: GB:ML7095; NID:gl47390; PIDN:AAA24436.1; PID:gl47391

A;Experimental source: strain K12

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;Finch, P.W.; Wilson, R.E.; Brown, K.; Hickson, I.D.; Emmerson, P.T.

Nucleic Acids Res. 14, 7695-7703, 1986

A;Title: Complete nucleotide sequence of the Escherichia coli ptr gene encoding protease

A;Reference number: A25765; UID:87040734; PMID:3534791

A;Accession: A25765

A;Molecule type: DNA

A;Residues: 1-962 <FIN>

A;Cross-references: GB:X06227; NID:g42560; PIDN:CAA29576.1; PID:g42561

R;Becker, A.B.; Roth, R.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 3835-3839, 1992

A;Title: An unusual active site identified in a family of zinc metalloendopeptidases.

A;Reference number: A38854; UID:92237263; PMID:1570301

A;Contents: annotation; active site

C;Genetics:

A;Gene: ptr

A;Map position: 61

C;Function:

A;Description: endopeptidase degrades small peptides [validated, UID:92237263]

A;Pathway: protein degradation

C;Superfamily: insulin-degrading enzyme (IDE)

C;Keywords: hydrolase; metalloproteinase; monomer; periplasmic space; protein degradatio

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-962/Product: pitirylisin #status experimental <MAT>

F;88,92/Binding site: zinc (His) #status experimental

F;91/Active site: Glu #status experimental

Query Match 42.6%; Score 43; DB 1; Length 962;

Best Local Similarity 61.1%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2 LDLEMLAPYIPMDDDFQL 19

Db 498 LSLPELNYPYP--DDFSL 513

RESULT 20

H85933

proteinase III [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Oct-2003

C;Accession: H85933

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe

Query Match 42.6%; Score 43; DB 2; Length 444;

Best Local Similarity 27.8%; Pred. No. 44;

Matches 5; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 LDLEMLAPYIPMDDDFQL 18

Db 326 NIDLDSTSPYLPLEEYK 343

RESULT 18

S62152

SFB2 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein N2505; protein YNL049c

C;Species: Saccharomyces cerevisiae

C;Date: 27-Apr-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004

C;Accession: S62152; S62977; S62974; S61095; S65102

R;Bergez, P.; Doignon, F.; Crouzet, M.

Yeast 11, 967-974, 1995

A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV

A;Reference number: S58711; UID:96021608; PMID:8533472

A;Accession: S62152

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-876 <BER>

A;Cross-references: UNIPROT:P53953; EMBL:U12141; NID:gl314216; PIDN:AAA99663.1; PID:gl05

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

R;Bergez, P.; Doignon, F.; Crouzet, M.

submitted to the Protein Sequence Database, April 1996

A;Reference number: S62975

A;Accession: S62977

A;Molecule type: DNA

A;Residues: 1-876 <BEW>

A;Cross-references: EMBL:Z71325; NID:gl301908; PID:e239676; PID:gl301909; MIPS:YNL049c

A;Experimental source: strain S288C

R;Nasr, F.; Becam, A.M.; Herbert, C.

submitted to the Protein Sequence Database, April 1996

A;Reference number: S62967

A;Accession: S62974

A;Molecule type: DNA

A;Residues: 1-544 <NAS>

A;Cross-references: EMBL:Z71325; MIPS:YNL049c

A;Experimental source: strain S288C

R;Nasr, F.; Becam, A.M.; Herbert, C.J.

submitted to the EMBL Data Library, December 1995

A;Description: The sequence of 12.8kb from the left arm of chromosome XIV reveals a sign

ne A4 hydrolase.

A;Reference number: S61095

A;Accession: S61095

A;Molecule type: DNA

A;Residues: 1-544 <NAW>

A;Cross-references: EMBL:X94547; NID:gl1149538; PID:e217483; PID:gl1149539

R;Nasr, F.; Becam, A.M.; Herbert, C.J.

Yeast 12, 493-499, 1996

A;Title: The sequence of 12.8 kb from the left arm of chromosome XIV reveals a sigma ele

otriene A(4) hydrolase.

A;Reference number: S65102; UID:96310629; PMID:8740423

A;Accession: S65102

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-544 <NAF>

A;Cross-references: EMBL:X94547; NID:gl1149538; PIDN:CAA64233.1; PID:gl1149539

C;Genetics:

A;Gene: SGB:SFB2

A;Cross-references: MIPS:YNL049c; SGD:S0004994

A;Map position: 14L

Query Match 42.6%; Score 43; DB 2; Length 876;

Best Local Similarity 50.0%; Pred. No. 98;

Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 YIPMDDDFQL 19

||:||||:

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoueis, K.; Apodaca, Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85933
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-962 <STO>
A:Cross-references: GB:AE005174; NID:g12517303; PIDN:AAG57932.1; GSPDB:GN00145; UWGP:241
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Superfamily: insulin-degrading enzyme (IDE)
Query Match 42.6%; Score 43; DB 2; Length 962;
Best Local Similarity 61.1%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
OY 2 LDLEMLAPYPMDDDFQL 19
| | | | | | | | | | | | | | | | | | | | | |
Db 498 LSLPELNPYIP--DDFSL 513
| | | | | | | | | | | | | | | | | | | | | |
RESULT 21
F91088
protease III [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F91088
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A95629; MUID:21156231; PMID:11258796
A:Accession: F91088
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-962 <HAY>
A:Cross-references: UNIPROT:Q8X6M8; GB:BA000007; PIDN:BA037101.1; PID:g13363150; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: Ecs3678
A:Superfamily: insulin-degrading enzyme (IDE)
Query Match 42.6%; Score 43; DB 2; Length 962;
Best Local Similarity 61.1%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
OY 2 LDLEMLAPYPMDDDFQL 19
| | | | | | | | | | | | | | | | | | | | | |
Db 498 LSLPELNPYIP--DDFSL 513
| | | | | | | | | | | | | | | | | | | | | |
RESULT 22
S15152
hypothetical protein 96 - phage pf1
C:Species: phage pf1
C>Date: 18-Feb-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C:Accession: S15152; S20823
R:Hill, D.P.; Short, N.J.; Perham, R.N.; Petersen, G.B. J. Mol. Biol. 218, 349-364, 1991
A>Title: DNA sequence of the filamentous bacteriophage pf1.
A:Reference number: S15140; MUID:91186399; PMID:2010913
A:Accession: S15152
A:Molecule type: DNA
A:Residues: 1-96 <JMO>
A:Cross-references: UNIPROT:P25134; EMBL:X52107; NID:g14829; PIDN:CAA36340.1; PID:g14841
A:Experimental source: ATCC 25102-B1
Query Match 41.6%; Score 42; DB 2; Length 96;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 2 LDLEMLAPYPMDDDFQL 19
| | | | | | | | | | | | | | | | | | | | | |
Db 498 LSLPELNPYIP--DDFSL 513
| | | | | | | | | | | | | | | | | | | | | |
RESULT 23
G69380
hypothetical protein AF1047 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
A:Accession: G69380
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, A.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69380
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-214 <KLE>
A:Cross-references: UNIPROT:O29215; GB:AE001030; GB:AE000782; NID:g2689353; PIDN:AAB9019
Query Match 41.6%; Score 42; DB 2; Length 214;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 1 LDLEMLAPYPMDDDFQ 18
| | | | | | | | | | | | | | | | | | | | | |
Db 126 DMDFEDLQGEIPLDADEQ 143
| | | | | | | | | | | | | | | | | | | | | |
RESULT 24
B6AG55
virB5 protein precursor - Agrobacterium tumefaciens plasmids pTi15955 and pTiA6
N:Alternate names: virB6 protein
C:Species: Agrobacterium tumefaciens
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
A:Accession: S00782; F28621; F27127
R:Thompson, D.V.; Melchers, L.S.; Idler, K.B.; Schilperoort, R.A.; Hooykaas, P.J.J. Nucleic Acids Res. 16, 4621-4636, 1988
A>Title: Analysis of the complete nucleotide sequence of the Agrobacterium tumefaciens virB5 protein precursor
A:Reference number: S00777; MUID:88247765; PMID:2837739
A:Accession: S00782
A:Molecule type: DNA
A:Residues: 1-220 <THO>
A:Cross-references: UNIPROT:P05355; EMBL:X06826; NID:g39195; PIDN:CAA29976.1; PID:g39206
A:Experimental source: strain 15955, plasmid pTi15955
R:Ward, J.E.; Akiyoshi, D.E.; Regier, D.; Datta, A.; Gordon, M.P.; Neester, E.W. J. Biol. Chem. 263, 5804-5814, 1988
A>Title: Characterization of the virB operon from an Agrobacterium tumefaciens Ti plasmid
A:Reference number: A28621; MUID:88186901; PMID:3281947
A:Accession: F28621
A:Molecule type: DNA
A:Residues: 1-220 <WAR>
A:Cross-references: GB:J03216; NID:g1196971; PIDN:AAA88650.1; PID:g1196977
A:Experimental source: plasmid pTiA6
A>Note: The authors translated the codon TTT for residue 25 as Pro
A>Note: this sequence was designated ORF 6 in this reference
R:Ward, J.E.; Akiyoshi, D.E.; Regier, D.; Datta, A.; Gordon, M.P.; Neester, E.W. J. Biol. Chem. 265, 4768, 1990
A:Reference number: A35737; MUID:90170994; PMID:2307685
A:Contents: annotation; erratum
A>Note: this sequence was designated ORF 6 in this reference
C:Genetics:
A:Gene: plasmid
A:Superfamily: tumor-inducing plasmid pTiC58 virB5 protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-220/Product: virB6 protein #status predicted <WAT>
Query Match 41.6%; Score 42; DB 1; Length 220;

Best Local Similarity 61.5%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPM 13
||| ||| : ||
Db 81 DLDNEMFSRPFM 93
||| ||| : ||

RESULT 25
H95920
probable membrane-anchored glycosyltransferase protein SMB21053 [imported] - Sinorhizobium
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95920
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-Kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H95920
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <KUR>
A;Cross-references: UNIPROT:Q92VVR7; GB:AL591985; PIDN:CAC49032.1; PID:gl5140517; GSPDB:G
A;Experimental source: Strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB21053
A;Genome: plasmid

Query Match 41.6%; Score 42; DB 2; Length 416;
Best Local Similarity 41.2%; Pred. No. 59;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDF 17
||| : ||| : ||
Db 238 DVELRIAGFSPPLPVD 254
||| : ||| : ||

RESULT 26
D96981
sugar ABC transporter, periplasmic sugar-binding protein CAC0662 [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: D96981
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D96981
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <KUR>
A;Cross-references: UNIPROT:Q97LA0; GB:AE001437; PIDN:AAK78639.1; PID:gl5023538; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0662

Query Match 41.6%; Score 42; DB 2; Length 451;
Best Local Similarity 64.3%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 LEMLAPYIPMDDDF 17
||| ||| ||| |||
Db 120 LEDLKPYEKDKDF 133
||| ||| ||| |||

RESULT 27

F96981

sugar-binding periplasmic protein [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: F96981

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: F96981

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-452 <KUR>

A;Cross-references: UNIPROT:Q97L98; GB:AE001437; PIDN:AAK78641.1; PID:gl5023540; GSPDB:G

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC0664

Query Match 41.6%; Score 42; DB 2; Length 452;

Best Local Similarity 64.3%; Pred. No. 65;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 LEMLAPYIPMDDDF 17

||| ||| ||| |||

Db 121 LEDLKPYEKDKDF 134

||| ||| ||| |||

RESULT 28

H84210

hypothetical protein Vng0525c [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: H84210

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S

; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li,

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: H84210

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-474 <STO>

A;Cross-references: UNIPROT:Q9HRV6; GB:AE004437; NID:gl0580126; PIDN:AAG19052.1; GSPDB:G

C;Genetics:

A;Gene: VNG0525C

C;Superfamily: Methanobacterium thermoautotrophicum ABC transporter Ycf24

Query Match 41.6%; Score 42; DB 2; Length 474;

Best Local Similarity 50.0%; Pred. No. 68;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDDF 16

||| : ||| : ||| |||

Db 77 ELDIEIIVPYIRPDVD 92

||| : ||| : ||| |||

RESULT 29

F95191

endopeptidase O [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: F95191

R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umavam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

naon, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357203; PMID:11463516
A:Accession: F95191
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-630 <KUR>
A:Cross-references: UNIPROT:Q97PH0; GB:AE005672; PIDN:AAK75727.1; PID:g14973138; GSPDB:G14973138
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI647
C:Superfamily: neprilysin

Query Match 41.6%; Score 42; DB 2; Length 630;
Best Local Similarity 43.8%; Pred. No. 96;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DLEMLAPYIPMDDDFQ 18
 | : || :| :|| :|
Db 219 DFKKFAPALPLDDEFFK 234

RESULT 30

B98058
 endopeptidase O (EC 3.4.24.-) [imported] - Streptococcus pneumoniae (strain R6)
 C/Species: Streptococcus pneumoniae
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C/Accession: B98058
 R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A/Reference number: A97872; MUID:21429245; PMID:11544234
 A/Accession: B98058
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-630 <KUR>
 A/Cross-references: UNIPROT:Q8DNW9; GB:AE007317; PIDN:AAL00295.1; PID:G15459150; GSPDB:G
 C/Genetics:
 A/Gene: pepo
 C/Supfamily: neprilysin
 C/Keywords: hydrolase; metalloproteinase

```
Query Match      41.6%; Score 42; DB 2; Length 630;
Best Local Similarity 43.8%; Pred. No. 96;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

Qy 3 DLEMLAPYIPMDDDFQ 18
| : | : | : | : | :
Db 219 DFKKFAPALPLDDFFK 234

RESULT 31

S38361
calpain (EC 3.4.22.17) II large chain - rat
N;Alternate names: calpain II 80K chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S38361; S08650; S39751
R;DeLuca, C.I.; Davies, P.L.; Samis, J.A.; Elce, J.S.
Biochim. Biophys. Acta 1216, 81-93, 1993
A;Title: Molecular cloning and bacterial expression of cDNA for rat calpain II 80 kDa su
A;Reference number: S38361; MUID:94032492; PMID:8218419
A;Accession: S38361
A;Molecule type: mRNA
A;Residues: 1-700
A;Cross-references: UNIPROT:Q07009; EMBL:L09120; NID:g402665; PIDN:AAA16327.1; PID:g40266
R;Samis, J.A.; Back, D.W.; Graham, E.J.; Elce, J.S.
submitted to the EMBL Data Library, February 1990
A;Reference number: S08650
A;Accession: S08650
A;Molecule type: DNA

```

A;Residues: 380-439 <SAM>
A;Cross-references: EMBL:RX51772
C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain
C;Keywords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer; hyc
F:75-327/Domain: calpain catalytic domain homology <CALP>
F:529-560/Domain: calmodulin repeat homology <CALP>
F:529-560/Domain: calmodulin repeat homology <EF1>
F:572-604/Domain: calmodulin repeat homology <EF2>
F:605-634/Domain: calmodulin repeat homology <EF3>
F:637-669/Domain: calmodulin repeat homology <EF4>
F:105,262,286/Active site: Cys, His, Asn #status predicted

Query Match 41.6%; Score 42; DB 2; Length 700;
Best Local Similarity 47.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LDLEMLAPVIPMDDDFQ 18
| : | : | : | : |
Db 116 LNEILARVPLDQSFQ 132

RESULT 32
A27602
complement C3 - rabbit (fragment)
N;Contents: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A27602

```

Immunol. Invest. 15, 365-378, 1986
A;Title: Nucleotide sequence of cDNA
A;Reference number: A27602; MUID:87
A;Accession: A27602

A;Molecule type: mRNA
A;Accession: A27602
A;Residues: 1-726 <KUS>
A;Cross-references: UNIPROT:P12247; GB:M32434; NID:G164862; PID:AAA31190.1; PID:G164863
C;Comment: Complement C3 contains two chains, formed by removal of four residues and four alternative complement pathways, releases the C3a anaphylatoxin from the amino end of the native-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign particles classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by protein C.
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein,

```
Query Match      41.6%; Score 42; DB 2; Length 726;
Best Local Similarity 38.9%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```

Qy 2 LDLEMLAPYIPMDDDFQL 19
||: |: ::| |||
Db 466 LDISMMTGFVPDTHDNL 483

RESULT 33

AC0865 Protease III precursor (pitirilysin) [imported] - *Salmonella enterica* subsp. *enterica* sero
C/Species: *Salmonella enterica* subsp. *enterica* serovar typhi
A/Note: this species has also been called *Salmonella typhi*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Oct-2003
R/Accession: AC0865
C/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AC0865
A/Status: preliminary
A/Molecule type: DNA
A/Molecule type: DNA
A/Residues: 1-962 <PAR>
A/Cross-references: CB:AL153382; PTDN:CAD02819.1; PID:gl16504073; GSPDB:GN00176

C;Genetics:
A;Gene: STY3133
C;Superfamily: Insulin-degrading enzyme (IDE)

Query Match 41.6%; Score 42; DB 2; Length 962;
Best Local Similarity 61.1%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 2 LDEMLAPYIPMDDDFQL 19
| | | | |
Db 498 LSLPELNPYP--DDFTL 513

RESULT 34
E83327
conserved hypothetical protein PA2542 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83327
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, J.M.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
adman, S.; Yuan, Y.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: E83327
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1221 <STO>
A;Cross-references: UNIPROT:Q91OU2; GB:AB004682; GB:AB004091; NID:g9948598; PIDN:AAG0593
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2542
C;Superfamily: ytfN protein

Query Match 41.6%; Score 42; DB 2; Length 1221;
Best Local Similarity 41.2%; Pred. No. 2.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LDEMLAPYIPMDDDFQ 18
| | | : | : | : |
Db 821 LDLSLARFPVPMVEKLG 837

RESULT 35
F90608
ABC transporter permease protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90608
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2599 <Kur>
A;Cross-references: UNIPROT:Q98PE9; GB:AL445566; PID:gl4090189; PIDN:CAC13947.1; GSPDB:C98PDB.1; GSPDB:C98PDB.1; GSPDB:C98PDB.1; GSPDB:C98PDB.1
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 7740
A;Genetic code: SGC3

Query Match 41.6%; Score 42; DB 2; Length 2599;
Best Local Similarity 42.9%; Pred. No. 5.2e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LEMLAPYIPMDDDF 17
| : | | | : | : |
Db 1144 VELLKKYLPLEGDF 1157

C:Genetics:
A:Gene: N-myc
A:Introns: 243/1
C:Superfamily: myc transforming protein; myc transforming protein homology
C:Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein; transforming protein
F:11-441/Domain: myc transforming protein homology <MYC>
F:410-436/Region: leucine zipper motif

Query Match 41.1%; Score 41.5; DB 1; Length 441;
Best Local Similarity 45.0%; Pred. No. 76;
Matches 9; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DLDLEMLAP-YIPMDDDFQL 19
|||: |||: |||: |||:
Db 10 DLEFDSLOPCFYFDEDDFYL 29

RESULT 39
G70090
hypothetical protein yyccs - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G70090
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Togmoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
C:Accession: G70090
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-137 <KUN>
A:Cross-references: UNIPROT:Q45603; GB:Z99124; GB:AL009126; NID:G2636442; PIDN:CAB16061.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yyccs
C:Superfamily: Bacillus subtilis hypothetical protein yyccs

Query Match 40.6%; Score 41; DB 2; Length 137;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DLEMLAPYIPMDDD 16
|||: |||: |||:
Db 36 DLEIYANYLQMHDD 49

RESULT 40
TVRTBM
transforming protein B-myc - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C:Accession: A45502; A31198
R:Asker, C.; Steinitz, M.; Andersson, K.; Suemegi, J.; Klein, G.; Ingvarsson, S.
Oncogene 4, 1523-1527, 1989
A:Title: Nucleotide sequence of the rat B-myc gene.
A:Reference number: A45502; MUID:90082428; PMID:2687773
C:Accession: A45502
A:Molecule type: DNA
A:Residues: 1-178 <ASK>
A:Cross-references: UNIPROT:P15063; GB:X17455; NID:G55830; PIDN:CAA35499.1; PID:G55831
A>Note: the authors translated the codon CAC for residue 173 as Gln

R:Ingvarsson, S.; Asker, C.; Axelson, H.; Klein, G.; Suemegi, J.
Mol. Cell. Biol. 8, 3168-3174, 1988
A:Title: Structure and expression of B-myc, a new member of the myc gene family.
A:Reference number: A31198; MUID:89096504; PMID:2850482
A:Accession: A31198
A:Molecule type: mRNA
A:Residues: 1-120 <ING>
C:Comment: The sequence is related to the amino end of the myc protein. It is missing t
ion.
C:Genetics:
A:Gene: B-myc
C:Superfamily: transforming protein B-myc; myc transforming protein homology
C:Keywords: DNA binding; transforming protein
F:14-178/Domain: myc transforming protein homology #status atypical <MYC>

Query Match 40.6%; Score 41; DB 1; Length 178;
Best Local Similarity 43.8%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DLDLEMLAPYIPMDDD 16
|||: |||: |||:
Db 13 DLDYDSVQPYFMCDD 28

RESULT 41
S37695
calcium-binding protein, vitamin D-dependent - fruit fly (Drosophila melanogaster)
N:Alternate names: calbindin-32
C:Species: Drosophila melanogaster
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
R:Reifegerste, R.; Grimm, S.; Albert, S.; Lipski, N.; Heimbeck, G.; Hofbauer, A.; Pflug
J. Neurosci. 13, 2186-2198, 1993
A:Title: An invertebrate calcium-binding protein of the calbindin subfamily: protein str
A:Reference number: S37695; MUID:93240238; PMID:8478695
A:Accession: S37695
A:Molecule type: mRNA
A:Residues: 1-310 <REI>
A:Cross-references: UNIPROT:P41044; EMBL:X68566; NID:G396506; PIDN:CAA48566.1; PID:G3965
C:Genetics:
A:Gene: FlyBase:Cbps53E
A:Cross-references: FlyBase:FBgn0004580
A:Map position: 2 53E
C:Superfamily: calretinin; calmodulin repeat homology
C:Keywords: calcium binding; duplication; EF hand; vitamin D
F:35-67/Domain: calmodulin repeat homology <EF1>
F:84-117/Domain: calmodulin repeat homology #status atypical <EF2>
F:131-163/Domain: calmodulin repeat homology <EF3>
F:177-209/Domain: calmodulin repeat homology <EF4>
F:224-256/Domain: calmodulin repeat homology <EF5>
F:48-50-52-54-59/Binding site: calcium (asp, asp, asp, Tyr, Glu) #status predicted
F:144,146,148,150,155/Binding site: calcium (asp, asp, asp, Ser, Tyr, Glu) #status predicted
F:190,192,194,196,201/Binding site: calcium (asp, asp, asp, Arg, Glu) #status predicted
F:237,239,241,243,248/Binding site: calcium (asp, asp, Ser, Thr, Glu) #status predicted

Query Match 40.6%; Score 41; DB 1; Length 310;
Best Local Similarity 38.9%; Pred. No. 60;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LDLEMLAPYIPMDDDFQL 19
|||: |||: |||: |||:
Db 105 IDIRELAQLPMENFLL 122

RESULT 42
B5552
trans-o-hydrobenzylidenepyruvate hydratase aldolase - Pseudomonas putida plasmid NAH7
C:Species: Pseudomonas putida
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C:Accession: B5552
R:Eaton, R.W.
J. Bacteriol. 176, 7757-7762, 1994
A:Title: Organization and evolution of naphthalene catabolic pathways: sequence of the D

from the NAH7 plasmid.
A:Reference number: A55552; MUID:95095951; PMID:8002605
A:Accession: B55552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <EAT>
A:Cross-references: UNIPROT:Q51947; GB:U09057; NID:G483790; PIDN:AAA66357.1; PID:G483792
C:Genetics:
A:Gene: nahE
A:Genome: plasmid
C:Superfamily: dihydrodipicolinate synthase

Query Match 40.6%; Score 41; DB 2; Length 331;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 10; Conservative 5; Mismatches 1; Indels 4; Gaps 2;

QY 1 DLDLEMLAP--YIPMDDDF 17
Db 191 DLDLK-LAPNIRFLPHEDDY 209
||||: |||: ||: |||:

RESULT 43
E64070
histidinol-phosphate transaminase (EC 2.6.1.9) - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: E64070
R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: E64070
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <TIGR>
A:Cross-references: UNIPROT:P44423; GB:U32730; GB:L42023; NID:G3212191; PIDN:AAC22129.1;
A:Note: named as homolog to a protein from Escherichia coli
C:Superfamily: histidinol-phosphate aminotransferase
C:Keywords: aminotransferase; histidine biosynthesis

Query Match 40.6%; Score 41; DB 1; Length 367;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 MLAPYIPMDDDFQL 19
Db 134 VLKTVPLTDDFQL 147
||: ||: |||

RESULT 44
G71633
ADP, ATP carrier protein (tlc5) RP739 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: G71633
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: G71633
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-500 <AND>
A:Cross-references: UNIPROT:O05962; GB:AJ235273; GB:AJ235269; NID:G3861237; PIDN:CAA1516
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: tlc5; RP739
C:Superfamily: rickettsial-type ATP/ADP translocase

Query Match 40.6%; Score 41; DB 2; Length 500;

Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 DLDLEMLAPYIPMDDDFQ 18
Db 417 DTSREML--YIPLDDELK 432
|||: |||: |||: |||:

RESULT 45
G84730
Mutator-like transposase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84730
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; L.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-684 <STO>
A:Cross-references: UNIPROT:Q9ZV55; GB:AE020293; NID:G3831469; PIDN:AAC69951.1; GSPDB:GN
C:Genetics:
A:Gene: At2g32250
A:Map position: 2

Query Match 40.6%; Score 41; DB 2; Length 684;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 EMLAPYIPMDDDF 17
Db 316 EMLNPFVSDQDF 328
|||: ||: |||

RESULT 46
S76766
hypothetical protein - Synecchocystis sp. (strain PCC 6803)
C:Species: Synecchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76766
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76766
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-713 <KAN>
A:Cross-references: UNIPROT:P74571; EMBL:D90916; GB:AB001339; NID:G1653715; PIDN:BAAL1867
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG
C:Superfamily: peptidyl-dipeptidase Dcp

Query Match 40.6%; Score 41; DB 2; Length 713;
Best Local Similarity 53.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DLDLEMLAPYIPM 13
Db 368 DFDAELRPYPPL 380
|||: |||: |||:

RESULT 47
A89944
atanyl-tRNA synthetase [imported] - Staphylococcus aureus (strain N315)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 20:10:07; Search time 27.6667 Seconds
(without alignments)
51.265 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 95

Sequence: 1 DLDLEMLAXYIPMDDDFQL 19

Scoring table:

BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	19	4	US-09-959-873B-8
2	95	100.0	34	4	US-09-959-873B-9
3	95	100.0	54	4	US-09-438-833-13
4	95	100.0	116	4	US-09-438-833-8
5	95	100.0	288	4	US-09-438-833-9
6	95	100.0	301	4	US-09-438-833-10
7	95	100.0	311	4	US-09-438-833-7
8	95	100.0	532	4	US-09-949-016-7389
9	95	100.0	613	4	US-09-438-833-6
10	95	100.0	652	4	US-09-438-833-5
11	95	100.0	756	4	US-09-438-833-11
12	95	100.0	805	2	US-08-480-473B-4
13	95	100.0	805	3	US-08-915-213-4
14	95	100.0	805	3	US-09-235-217-4
15	95	100.0	805	5	PCT-US96-10251-4
16	95	100.0	810	1	US-08-785-241-7
17	95	100.0	813	4	US-09-438-833-12
18	95	100.0	826	1	US-08-785-241-6
19	95	100.0	826	3	US-08-480-473B-2
20	95	100.0	826	3	US-08-915-213-2
21	95	100.0	826	3	US-09-148-547-2
22	95	100.0	826	3	US-09-235-217-2
23	95	100.0	826	3	US-09-380-662-23
24	95	100.0	826	4	US-09-438-833-1
25	95	100.0	826	4	US-09-702-705-330
26	95	100.0	826	4	US-09-736-457-330
27	95	100.0	826	4	US-09-383-581-2

28	95	100.0	826	4	US-09-614-124B-330	Sequence 330, App
29	95	100.0	826	4	US-09-671-325-330	Sequence 330, App
30	95	100.0	826	4	US-09-589-184-330	Sequence 330, App
31	95	100.0	826	4	US-09-658-824-330	Sequence 330, App
32	95	100.0	826	4	US-09-959-873B-18	Sequence 18, Appl
33	95	100.0	826	4	US-09-949-016-6089	Sequence 6089, Ap
34	95	100.0	826	4	US-09-967-388-4	Sequence 4, Appl
35	95	100.0	826	5	PCT-US96-10251-2	Sequence 2, Appl
36	95	100.0	827	4	US-09-919-039-149	Sequence 149, App
37	83	87.4	19	4	US-09-972-784-5	Sequence 5, Appl
38	70.5	74.2	205	3	US-09-374-454-2	Sequence 2, Appl
39	70.5	74.2	870	1	US-08-785-241-4	Sequence 4, Appl
40	70.5	74.2	870	3	US-09-374-454-6	Sequence 6, Appl
41	70.5	74.2	875	1	US-08-785-241-5	Sequence 5, Appl
42	48	50.5	143	4	US-09-270-767-42631	Sequence 42631, A
43	48	50.5	182	4	US-09-248-796A-20521	Sequence 20521, A
44	48	50.5	1507	4	US-09-914-259-37	Sequence 37, Appl
45	46	48.4	98	4	US-09-543-681A-8077	Sequence 8077, Ap
46	43	45.3	358	4	US-09-270-767-45720	Sequence 45720, A
47	43	45.3	703	2	US-08-835-099A-1	Sequence 1, Appl
48	43	45.3	703	3	US-09-157-349-1	Sequence 1, Appl
49	43	45.3	712	2	US-08-835-099A-2	Sequence 2, Appl
50	43	45.3	712	3	US-09-157-349-2	Sequence 2, Appl
51	43	45.3	1087	3	US-09-252-991A-28584	Sequence 28584, A
52	42	44.2	201	4	US-09-489-039A-7210	Sequence 7210, Ap
53	42	44.2	217	4	US-09-198-452A-656	Sequence 656, App
54	42	44.2	237	4	US-09-438-185A-620	Sequence 620, App
55	42	44.2	347	4	US-09-489-039A-7824	Sequence 7824, Ap
56	41	43.2	275	4	US-09-328-352-7814	Sequence 7814, Ap
57	41	43.2	700	4	US-09-308-345A-46	Sequence 46, Appl
58	41	43.2	895	4	US-09-489-039A-12499	Sequence 12499, A
59	41	43.2	900	4	US-09-248-796A-16848	Sequence 16848, A
60	40	42.1	61	4	US-09-513-999C-4471	Sequence 4471, Ap
61	40	42.1	147	3	US-08-965-762-30	Sequence 30, Appl
62	40	42.1	147	4	US-09-911-927-30	Sequence 30, Appl
63	40	42.1	147	4	US-09-911-882-30	Sequence 30, Appl
64	40	42.1	147	4	US-09-911-888-30	Sequence 30, Appl
65	40	42.1	436	4	US-09-252-991A-17273	Sequence 17273, A

ALIGNMENTS

RESULT 1
US-09-959-873B-8
; Sequence 8, Application US/09959873B
; Patent No. 6787226
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-09-959-873B-8
Query Match 100.0%; Score 95; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e-08;

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Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2
US-09-959-873B-9
; Sequence 9, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GH00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-959-873B-9

Query Match 100.0%; Score 95; DB 4; Length 34;
Best Local Similarity 94.7%; Pred. No. 2.3e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 3
US-09-438-833-13
; Sequence 13, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
US-09-438-833-13

Query Match 100.0%; Score 95; DB 4; Length 54;
Best Local Similarity 94.7%; Pred. No. 3.9e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 26 DLDLEMLAPYIPMDDDFQL 44

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 95; DB 4; Length 116;
Best Local Similarity 94.7%; Pred. No. 9.9e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 4
US-09-438-833-8
; Sequence 8, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
US-09-438-833-8

Query Match 100.0%; Score 95; DB 4; Length 116;
Best Local Similarity 94.7%; Pred. No. 9.9e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 5
US-09-438-833-9
; Sequence 9, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
US-09-438-833-9

Query Match 100.0%; Score 95; DB 4; Length 288;
Best Local Similarity 94.7%; Pred. No. 3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 6
US-09-438-833-10
; Sequence 10, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 10
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-826 of human HIF-1 alpha
US-09-438-833-10

Query Match 100.0%; Score 95; DB 4; Length 301;
Best Local Similarity 94.7%; Pred. No. 3.1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 7
US-09-438-833-7
; Sequence 7, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 331-641 of human HIF-1 alpha
US-09-438-833-7

Query Match 100.0%; Score 95; DB 4; Length 311;
Best Local Similarity 94.7%; Pred. No. 3.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 226 DLDLEMLAPYIPMDDDFQL 244

RESULT 8
US-09-949-016-7389
; Sequence 7389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7389
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7389

Query Match 100.0%; Score 95; DB 4; Length 532;
Best Local Similarity 94.7%; Pred. No. 6.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 262 DLDLEMLAPYIPMDDDFQL 280

RESULT 9
US-09-438-833-6
; Sequence 6, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-438-833-6

Query Match 100.0%; Score 95; DB 4; Length 613;
Best Local Similarity 94.7%; Pred. No. 7.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 343 DLDLEMLAPYIPMDDDFQL 361

RESULT 10
US-09-438-833-5
; Sequence 5, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-652 of human HIF-1 alpha
US-09-438-833-5

Query Match 100.0%; Score 95; DB 4; Length 652;
Best Local Similarity 94.7%; Pred. No. 8e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 11
US-09-438-833-11
; Sequence 11, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants

FILE REFERENCE: 1848
CURRENT APPLICATION NUMBER: US/09/438,833
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 756
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Subdomain
OTHER INFORMATION: 71-826 of human HIF-1 alpha
US-09-438-833-11

Query Match 100.0%; Score 95; DB 4; Length 756;
Best Local Similarity 94.7%; Pred. No. 9.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 486 DLDLEMLAPYIPMDDDFQL 504

RESULT 12

US-08-480-473B-4
Sequence 4, Application US/08480473B
Patent No. 5982914
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,473B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-473B-4

Query Match 100.0%; Score 95; DB 2; Length 805;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 535 DLDLEMLAPYIPMDDDFQL 553

RESULT 13

US-08-915-213-4
Sequence 4, Application US/08915213
Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-213-4

Query Match 100.0%; Score 95; DB 3; Length 805;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 535 DLDLEMLAPYIPMDDDFQL 553

RESULT 14

US-09-235-217-4
Sequence 4, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:

APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,217

;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/480,473
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07265/053001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619/678-5070
;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 805 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-235-217-4

Query Match 100.0%; Score 95; DB 3; Length 805;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 535 DLDLEMLAPYIPMDDDFOL 553

RESULT 15
PCT-US96-10251-4
;; Sequence 4, Application PC/TUS9610251
;; GENERAL INFORMATION:
;; APPLICANT: The Johns Hopkins University School of Medicine
;; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSER: Fish & Richardson P.C.
;; STREET: 4225 Executive Square, Suite 1400
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10251
;; FILING DATE: 06-JUN-1996
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07265/053001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619/678-5070
;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 805 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US96-10251-4

Query Match 100.0%; Score 95; DB 5; Length 805;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 535 DLDLEMLAPYIPMDDDFOL 553
RESULT 16
US-08-785-241-7
;; Sequence 7, Application US/08785241
;; Patent No. 5695963
;; GENERAL INFORMATION:
;; APPLICANT: McKnight, Steven L.
;; APPLICANT: Russell, David W.
;; APPLICANT: Tian, Rui
;; TITLE OF INVENTION: Endothelial PAS Domain Protein
;; NUMBER OF SEQUENCES: 7
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/785,241
;; FILING DATE: 17-JAN-1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A.
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: UTSD:1229
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 810 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-785-241-7

Query Match 100.0%; Score 95; DB 1; Length 810;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 543 DLDLEMLAPYIPMDDDFOL 561

RESULT 17
US-09-438-833-12
;; Sequence 12, Application US/09438833
;; Patent No. 6436654
;; GENERAL INFORMATION:
;; APPLICANT: Pharmacia & Upjohn
;; TITLE OF INVENTION: Protein variants
;; FILE REFERENCE: 1848
;; CURRENT APPLICATION NUMBER: US/09/438,833
;; CURRENT FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 12
;; LENGTH: 813
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-915-213-2

Query Match 100.0%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574
|||||:|||||

RESULT 21
US-148-547-2
; Sequence 2, Application US/09148547
; Patent No. 6124131
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/148,547
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-148-547-2

Query Match 100.0%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574
|||||:|||||

RESULT 22
US-09-235-217-2
; Sequence 2, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; CITY: La Jolla
; STREET: 4225 Executive Square, Suite 1400
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/235,217
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-217-2

Query Match 100.0%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574
|||||:|||||

RESULT 23
US-09-380-662-23
; Sequence 23, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-23

Query Match 100.0%; Score 95; DB 3; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574
|||||:|||||

RESULT 24
US-09-438-833-1
; Sequence 1, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

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; VOLUME: 92
; PAGES: 5510-5514
; DATABASE ACCESSION NUMBER: GenBank U22431
; DATABASE ENTRY DATE: 1995-06-28
US-09-438-833-1

Query Match          100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 25
US-09-702-705-330
; Sequence 330, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1933
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-330

Query Match          100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 26
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match          100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 27
US-09-383-581-2
; Sequence 2, Application US/09383581
; Patent No. 6562799
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/09/383,581
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-581-2

Query Match          100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 28
US-09-614-124B-330
; Sequence 330, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-330

Query Match          100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
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Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574
    |||||:|||||

RESULT 29
US-09-671-325-330
; Sequence 330, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-330

Query Match 100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574
    |||||:|||||

RESULT 30
US-09-589-184-330
; Sequence 330, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-330

Query Match 100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574
    |||||:|||||

RESULT 31
US-09-658-824-330
; Sequence 330, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-330

Query Match 100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574
    |||||:|||||

RESULT 32
US-09-959-873B-18
; Sequence 18, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-873B-18

Query Match 100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
    |||||:|||||
Db 556 DLDLEMLAPYIPMDDDFQL 574
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Db      556 DLDLEMLAPYIPMDDDFOL 574

RESULT 33
US-09-949-016-6089
; Sequence 6089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6089
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6089

Query Match      100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||

Db      556 DLDLEMLAPYIPMDDDFOL 574

RESULT 34
US-09-967-388-4
; Sequence 4, Application US/09967388
; Patent No. 6838430
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; WOUND HEALING
; FILE REFERENCE: UC077-001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match      100.0%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||

Db      556 DLDLEMLAPYIPMDDDFOL 574

RESULT 35
PCT-US96-10251-2
; Sequence 2, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10251-2

Query Match      100.0%; Score 95; DB 5; Length 826;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||

Db      556 DLDLEMLAPYIPMDDDFOL 574

RESULT 36
US-09-919-039-149
; Sequence 149, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CD1
US-09-919-039-149

Query Match      100.0%; Score 95; DB 4; Length 827;
Best Local Similarity 94.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||

Db      557 DLDLEMLAPYIPMDDDFOL 575

RESULT 37
US-09-972-784-5
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Query Match          74.2%; Score 70.5; DB 3; Length 870;
Best Local Similarity 75.0%; Pred. No. 0.0086;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy      1  LDLEMLAXYPMD-DDFQL 19
          :| | | | | | | | | | | | | | | |
Db      523  ELDETLAPYPMGDGDFQL 542

RESULT 41
US-08-785-241-5
; Sequence 5, Application US/08785241
; Patent No. 5695963

```

GENERAL INFORMATION:
APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
TITLE OF INVENTION: Endothelial PAS Domain Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,241
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-241-5

Query Match 74.2%; Score 70.5; DB 1; Length 875;
Best Local Similarity 75.0%; Pred. No. 0.0087;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAXYIPMD-DDFOL 19
:|||||:|||||:|||||
Db 523 ELDLETLAPYIPMDGEDFOL 542

RESULT 42
US-09-270-767-42631
Sequence 42631, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42631
LENGTH: 143
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-42631

Query Match 50.5%; Score 48; DB 4; Length 143;
Best Local Similarity 64.3%; Pred. No. 3.6;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MLAXYIPMDDDFOL 19
|:|:|:|:|:|:|:|
Db 93 MRAPYIPIDDDMPL 106

RESULT 43
US-09-248-796A-20521
Sequence 20521, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20521
LENGTH: 182
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20521

Query Match 50.5%; Score 48; DB 4; Length 182;
Best Local Similarity 72.7%; Pred. No. 4.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 MLAXYIPMDDD 16
|:|:|:|:|:|:|
Db 44 MLAGYLPFDDD 54

RESULT 44
US-09-914-259-37
Sequence 37, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 1507
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-914-259-37

Query Match 50.5%; Score 48; DB 4; Length 1507;
Best Local Similarity 64.3%; Pred. No. 62;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MLAXYIPMDDDFOL 19
|:|:|:|:|:|:|
Db 847 MRAPYIPIDDDMPL 860

RESULT 45
US-09-543-681A-8077
Sequence 8077, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706

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; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8077
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8077

Query Match      48.4%; Score 46; DB 4; Length 98;
Best Local Similarity 75.0%; Pred. No. 4.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 EMLAXYIPMDD 16
   |.:|.:|.:|
Db 87 ERLATLIPMDD 98

RESULT 46
US-09-270-767-45720
; Sequence 45720, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45720
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45720

Query Match      45.3%; Score 43; DB 4; Length 358;
Best Local Similarity 42.9%; Pred. No. 68;
Matches 9; Conservative 6; Mismatches 4; Indels 2; Gaps 1;

QY 1 DLDLEMLAXYIP--MDDPQL 19
   :.:|.:|.:|.:|
Db 204 EYETQLAMAVPPVDDDDQL 224

RESULT 47
US-08-835-099A-1
; Sequence 1, Application US/08835099A
; Patent No. 5874277
; GENERAL INFORMATION:
; APPLICANT: SHINTANI, Yasuuehi
; APPLICANT: NISHI, Kazunori
; APPLICANT: KAWAMOTO, Tomohiro
; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,099A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 083649/1996
; FILING DATE: 05-APR-1996
; APPLICATION NUMBER: 97105508.2
; FILING DATE: 03-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 47342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 703 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-835-099A-1

Query Match      45.3%; Score 43; DB 2; Length 703;
Best Local Similarity 47.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LDLEMLAXYIPMDDDFQ 18
   |.:|.:|.:|.:|
Db 116 LNEELLYRVPRDQDFQ 132

RESULT 48
US-09-157-349-1
; Sequence 1, Application US/09157349
; Patent No. 6068990
; GENERAL INFORMATION:
; APPLICANT: SHINTANI, Yasuuehi
; APPLICANT: NISHI, Kazunori
; APPLICANT: KAWAMOTO, Tomohiro
; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,349
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,099
; FILING DATE:
; APPLICATION NUMBER: 97105508.2
; FILING DATE: 03-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 47342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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OM protein - protein search, using sw model

Run on: February 8, 2005, 20:15:22 ; Search time 74.6667 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 95

Sequence: 1 DLDLEMLAXYIPMDDFQL 19

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Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/CTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	19	US-10-901-583-8	Sequence 8, Appli
2	95	100.0	20	US-10-101-662A-15	Sequence 15, Appl
3	95	100.0	20	US-10-287-670-15	Sequence 15, Appl
4	95	100.0	20	US-10-287-670-25	Sequence 25, Appl
5	95	100.0	34	US-10-901-583-9	Sequence 9, Appli
6	95	100.0	54	US-09-922-958-5	Sequence 5, Appli
7	95	100.0	409	US-10-425-833-8	Sequence 8, Appli
8	95	100.0	466	US-10-425-833-9	Sequence 9, Appli
9	95	100.0	538	US-10-425-833-6	Sequence 6, Appli
10	95	100.0	542	US-10-264-049-2606	Sequence 2606, Ap
11	95	100.0	595	US-10-425-833-7	Sequence 7, Appli
12	95	100.0	632	US-10-425-833-10	Sequence 10, Appl
13	95	100.0	823	US-10-205-342-13	Sequence 13, Appl

14	95	100.0	826	9	US-09-922-958-4	Sequence 4, Appli
15	95	100.0	826	9	US-09-833-790-235	Sequence 235, App
16	95	100.0	826	9	US-09-736-457-330	Sequence 330, App
17	95	100.0	826	9	US-09-902-941-330	Sequence 330, App
18	95	100.0	826	9	US-09-843-626-330	Sequence 330, App
19	95	100.0	826	10	US-09-967-388-4	Sequence 4, Appli
20	95	100.0	826	10	US-09-476-300-330	Sequence 330, App
21	95	100.0	826	13	US-10-028-158-23	Sequence 23, Appl
22	95	100.0	826	13	US-10-101-812-10	Sequence 10, Appl
23	95	100.0	826	14	US-10-101-662A-9	Sequence 9, Appli
24	95	100.0	826	14	US-10-101-816-2	Sequence 2, Appli
25	95	100.0	826	14	US-10-017-754-330	Sequence 330, App
26	95	100.0	826	14	US-10-115-987B-14	Sequence 14, Appl
27	95	100.0	826	14	US-10-287-670-9	Sequence 9, Appli
28	95	100.0	826	14	US-10-113-872-330	Sequence 330, App
29	95	100.0	826	14	US-10-423-419-2	Sequence 2, Appli
30	95	100.0	826	15	US-10-283-017-330	Sequence 330, App
31	95	100.0	826	16	US-10-901-583-18	Sequence 18, Appl
32	95	100.0	827	10	US-09-919-039-149	Sequence 149, App
33	95	100.0	827	14	US-10-247-671-137	Sequence 137, App
34	90	94.7	826	14	US-10-101-816-5	Sequence 5, Appli
35	90	94.7	826	14	US-10-101-816-6	Sequence 6, Appli
36	90	94.7	826	14	US-10-101-816-7	Sequence 7, Appli
37	83	87.4	19	14	US-10-313-551A-5	Sequence 5, Appli
38	83	87.4	19	14	US-10-313-551A-5	Sequence 5, Appli
39	81	85.3	297	15	US-10-296-115-933	Sequence 933, App
40	81	85.3	705	14	US-10-154-386-2	Sequence 2, Appli
41	70.5	74.2	205	14	US-10-121-235-2	Sequence 2, Appli
42	70.5	74.2	870	14	US-10-121-235-6	Sequence 6, Appli
43	63.5	66.8	870	14	US-10-101-816-4	Sequence 4, Appli
44	48	50.5	793	15	US-10-369-493-3670	Sequence 3670, Ap
45	48	50.5	800	15	US-10-369-493-22401	Sequence 22401, A
46	48	50.5	800	15	US-10-618-581-6	Sequence 6, Appli
47	48	50.5	994	15	US-10-618-581-8	Sequence 8, Appli
48	48	50.5	1507	14	US-10-080-608A-37	Sequence 37, Appl
49	48	50.5	1507	15	US-10-370-685-126	Sequence 126, App
50	47	49.5	707	14	US-10-149-823-2	Sequence 2, Appli
51	46	48.4	283	16	US-10-437-963-130267	Sequence 130267,
52	45	47.4	77	15	US-10-424-599-221970	Sequence 221970,
53	45	47.4	128	15	US-10-424-599-181430	Sequence 181430,
54	44	46.3	324	9	US-09-815-242-10978	Sequence 10978, A
55	44	46.3	324	15	US-10-424-599-209732	Sequence 209732,
56	43	45.3	143	15	US-10-425-114-48672	Sequence 48672, A
57	43	45.3	180	15	US-10-424-599-159596	Sequence 159596,
58	43	45.3	401	15	US-10-767-701-44861	Sequence 44861, A
59	43	45.3	703	15	US-10-275-107-44	Sequence 44, Appl
60	43	45.3	703	15	US-10-275-505-3	Sequence 3, Appli
61	43	45.3	727	16	US-10-437-963-110465	Sequence 110465,
62	43	45.3	865	15	US-10-618-581-7	Sequence 7, Appli
63	43	45.3	1194	16	US-10-437-963-110468	Sequence 110468,
64	42.5	44.7	474	15	US-10-282-122A-54581	Sequence 54581, A
65	42	44.2	136	15	US-10-424-599-250397	Sequence 250397,

ALIGNMENTS

RESULT 1

US-10-901-583-8
; Sequence 8, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; FILE REFERENCE: 3547 1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; PRIORITY FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959, 873
; PRIOR FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-10-901-583-8

Query Match 100.0%; Score 95; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.8e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
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Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2
US-10-101-662A-15
; Sequence 15, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-101-662A-15

Query Match 100.0%; Score 95; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 3
US-10-287-670-15
; Sequence 15, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009CIP1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-287-670-15

Query Match 100.0%; Score 95; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 4
US-10-287-670-25
; Sequence 25, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009CIP1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816

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; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-25

Query Match      100.0%; Score 95; DB 14; Length 20;
Best Local Similarity 94.7%; Pred. No. 3e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
   |||||:|||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 5
US-10-901-583-9
; Sequence 9, Application US/10901593
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-901-583-9

Query Match      100.0%; Score 95; DB 16; Length 34;
Best Local Similarity 94.7%; Pred. No. 5.6e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
   |||||:|||||
Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 6
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US-09-922-958-5
; Sequence 5, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-5

Query Match      100.0%; Score 95; DB 9; Length 54;
Best Local Similarity 94.7%; Pred. No. 9.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
   |||||:|||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 7
US-10-425-833-8
; Sequence 8, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-8

Query Match      100.0%; Score 95; DB 15; Length 409;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
   |||||:|||||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 8
US-10-425-833-9
; Sequence 9, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
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; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 466
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

Query Match 100.0%; Score 95; DB 15; Length 466;
Best Local Similarity 94.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
DB 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 9
US-10-425-833-6
; Sequence 6, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-6

Query Match 100.0%; Score 95; DB 15; Length 538;
Best Local Similarity 94.7%; Pred. No. 1.4e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 10
US-10-264-049-2606
; Sequence 2606, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Bires et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 2606
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2606

Query Match 100.0%; Score 95; DB 15; Length 542;
Best Local Similarity 94.7%; Pred. No. 1.4e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
DB 272 DLDLEMLAPYIPMDDDFQL 290

RESULT 11
US-10-425-833-7
; Sequence 7, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 595
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-7

Query Match 100.0%; Score 95; DB 15; Length 595;
Best Local Similarity 94.7%; Pred. No. 1.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
DB 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 12
US-10-425-833-10
; Sequence 10, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 632
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-10

Query Match 100.0%; Score 95; DB 15; Length 632;

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Best Local Similarity 94.7%; Pred. No. 1.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 13
US-10-205-342-13
; Sequence 13, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Protein: hypoxia-inducible factor-1 alpha
US-10-205-342-13

Query Match 100.0%; Score 95; DB 14; Length 823;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 14
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US2002004879A1
; GENERAL INFORMATION:
; APPLICANT: FOELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACTOR-1
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-4

Query Match 100.0%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 556 DLDLEMLAPYIPMDDDFQL 574
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RESULT 15
US-09-833-790-235
; Sequence 235, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-235

Query Match 100.0%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 16
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 100.0%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 17
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 100.0%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 556 DLDLEMLAPYIPMDDDFQL 574
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US-09-902-941-330
; Sequence 330, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McRabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-330

Query Match 100.0%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 18
US-09-849-626-330
; Sequence 330, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-330

Query Match 100.0%; Score 95; DB 9; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 19
US-09-967-388-4

; Sequence 4, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match 100.0%; Score 95; DB 10; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 20
US-09-476-300-330
; Sequence 330, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-330

Query Match 100.0%; Score 95; DB 10; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFOL 19
|||||:|||||
Db 556 DLDLEMLAPYIPMDDDFOL 574

RESULT 21
US-10-028-158-23
; Sequence 23, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919

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; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-158-23

Query Match      100.0%; Score 95; DB 13; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLDLEMLAXYIPMDDDFQL 19
        |||||:|||||
Db       556 DLDLEMLAPYIPMDDDFQL 574

RESULT 22
US-10-101-812-10
; Sequence 10, Application US/10101812
; Publication No. US20020192737A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Pharmaceuticals and Methods for Treating Hypoxia and
; FILE REFERENCE: 20363-014
; CURRENT APPLICATION NUMBER: US/10/101,812
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
US-10-101-812-10

Query Match      100.0%; Score 95; DB 13; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLDLEMLAXYIPMDDDFQL 19
        |||||:|||||
Db       556 DLDLEMLAPYIPMDDDFQL 574

RESULT 23
US-10-101-662A-9
; Sequence 9, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-662A-9

Query Match      100.0%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLDLEMLAXYIPMDDDFQL 19
        |||||:|||||
Db       556 DLDLEMLAPYIPMDDDFQL 574

RESULT 24
US-10-101-816-2
; Sequence 2, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Mutains of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
US-10-101-812-10
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-2

Query Match 100.0%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 25

US-10-017-754-330
; Sequence 330, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fager, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-330

Query Match 100.0%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 26

US-10-115-987B-14
; Sequence 14, Application US/10115987B
; Publication No. US20030148521A1
; GENERAL INFORMATION:
; APPLICANT: Bell, John C.; Stojdl, David F.;
; APPLICANT: Gray, Douglas A.; Sonenberg,
; APPLICANT: Nahum, Lichty, Brian
; TITLE OF INVENTION: Conditionally Replicative and
; TITLE OF INVENTION: Conditionally Active Viruses
; FILE REFERENCE: 42630-0001
; CURRENT APPLICATION NUMBER: US/10/115,987B
; CURRENT FILING DATE: 2002-03-03
; PRIOR APPLICATION NUMBER: US60/281,781
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: EditPad
; SEQ ID NO 14
; LENGTH: 826
; TYPE: PRT
; ORGANISM: homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Wang et al.
; JOURNAL: Proceedings of the National Academy of Sciences
; VOLUME: 92
; PAGES: 5510-5514
; DATE: 1995
US-10-115-987B-14

Query Match 100.0%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 27

US-10-287-670-9
; Sequence 9, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-005C1P1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-9

Query Match 100.0%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||||:|||||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 28

; Sequence 330, Application US/10283017
 ; Publication No. US20030211510A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Watanabe, Yoshihiro

US-09-919-039-149
; Sequence 149, Application US/09919039
; Publication No. US20030108871A1

```
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
US-09-919-039-149

Query Match 100.0%; Score 95; DB 10; Length 827;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 33
US-10-247-671-137
; Sequence 137, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 137
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CD1
US-10-247-671-137

Query Match 100.0%; Score 95; DB 14; Length 827;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 34
US-10-101-816-5
; Sequence 5, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: 20363-008
```

```
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-5

Query Match 94.7%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 1.5e-05;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 35
US-10-101-816-6
; Sequence 6, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 826
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-6

Query Match          94.7%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 1.5e-05;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
    ||||| 1:|||||||
Db 556 DLDLEMAAAYIPMDDDFQL 574

RESULT 36
US-10-101-816-7
; Sequence 7, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-7

Query Match          94.7%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 1.5e-05;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
    ||||| 1:|||||||
Db 556 DLDLEMAAAYIPMDDDFQL 574

RESULT 37
US-10-313-643A-5
; Sequence 5, Application US/10313643A
; Publication No. US20030153503A1
; GENERAL INFORMATION:
; APPLICANT: Klaus, Stephen J.
; APPLICANT: Lin, Al Y.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
```

```
; APPLICANT: Arend, Michael P.
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: METHODS OF INCREASING ENDOGENOUS ERYTHROPOIETIN (EPO)
; FILE REFERENCE: FP0601 US
; CURRENT APPLICATION NUMBER: US/10/313,643A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-313-643A-5

Query Match          87.4%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.3e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
    ||||| 1:||||
Db 1 DLDLEALAPYIPADDDFQL 19

RESULT 38
US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
; APPLICANT: Guenzler-Pukall, Volkmar
; APPLICANT: Neff, Thomas B.
; APPLICANT: Wang, Qingjian
; APPLICANT: Arend, Michael
; APPLICANT: Flippin, Lee A.
; APPLICANT: Melekhov, Alexey G.
; TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
; FILE REFERENCE: FP0600 US
; CURRENT APPLICATION NUMBER: US/10/313,551A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/337,082
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/359,683
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/349,659
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/386,488
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-313-551A-5

Query Match          87.4%; Score 83; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.3e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
    ||||| 1:||||
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Db 1 LDLEALAPYIPADDDFQL 19
; APPLICANT: Hsieh, Chung-Ming
; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
; FILE REFERENCE: 05433/037001
; CURRENT APPLICATION NUMBER: US/10/121,235
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/374,454
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 60/096,515
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-121-235-2
Query Match 74.2%; Score 70.5; DB 14; Length 205;
Best Local Similarity 75.0%; Pred. No. 0.0037;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

RESULT 39
US-10-296-115-933
; Sequence 933, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 933
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-296-115-933
Query Match 85.3%; Score 81; DB 15; Length 297;
Best Local Similarity 88.9%; Pred. No. 0.00012;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 40
US-10-154-386-2
; Sequence 2, Application US/10154386
; Publication No. US20030026793A1
; GENERAL INFORMATION:
; APPLICANT: Angiogene Inc.
; TITLE OF INVENTION: HIPOXIA INDUCING FACTORS AND USES THEREOF FOR INDUCING ANGIOGENESIS
; FILE REFERENCE: 5600-81
; CURRENT APPLICATION NUMBER: US/10/154,386
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,630
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/354529
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-154-386-2
Query Match 85.3%; Score 81; DB 14; Length 705;
Best Local Similarity 88.9%; Pred. No. 0.00033;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 41
US-10-121-235-2
; Sequence 2, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Maemura, Koji
; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
; FILE REFERENCE: 05433/037001
; CURRENT APPLICATION NUMBER: US/10/121,235
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/374,454
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 60/096,515
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-121-235-6
Query Match 74.2%; Score 70.5; DB 14; Length 870;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

RESULT 42
US-10-121-235-6
; Sequence 6, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Maemura, Koji
; APPLICANT: Hsieh, Chung-Ming
; TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
; FILE REFERENCE: 05433/037001
; CURRENT APPLICATION NUMBER: US/10/121,235
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/374,454
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 60/096,515
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-121-235-6
Query Match 74.2%; Score 70.5; DB 14; Length 870;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

RESULT 43
US-10-101-816-4
; Sequence 4, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Mutelins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; APPLICANT: Maemura, Koji
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; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-4

Query Match 66.8%; Score 63.5; DB 14; Length 870;
Best Local Similarity 70.0%; Pred. No. 0.26;
Matches 14; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 DLDLEMLAXYIPMD-DDFQL 19

:|||||:|||||:|||||

Db 523 ELDTLAAYIPMDGEGFQL 542

RESULT 44

US-10-369-493-3670
; Sequence 3670, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3670
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(793)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3670

Query Match 50.5%; Score 48; DB 15; Length 793;
Best Local Similarity 72.7%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 MLAXYIPMDDDD 16

Db 277 MLAGYLPFDDDD 287

RESULT 45

US-10-369-493-22401
; Sequence 22401, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22401
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22401

Query Match 50.5%; Score 48; DB 15; Length 800;
Best Local Similarity 61.5%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MLAXYIPMDDDFQ 18

Db 245 MLAGYLPWDDHDE 257

RESULT 46

US-10-618-581-6
; Sequence 6, Application US/10618581
; Publication No. US20040077524A1
; GENERAL INFORMATION:
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR SELECTIVELY INHIBITING FUNGAL GROWTH
; FILE REFERENCE: 034536/0323
; CURRENT APPLICATION NUMBER: US/10/618,581
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,624
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-618-581-6

Query Match 50.5%; Score 48; DB 15; Length 800;
Best Local Similarity 61.5%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MLAXYIPMDDDFQ 18

Db 245 MLAGYLPWDDHDE 257

RESULT 47

US-10-618-581-8
; Sequence 8, Application US/10618581
; Publication No. US20040077524A1
; GENERAL INFORMATION:
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR SELECTIVELY INHIBITING FUNGAL GROWTH
; FILE REFERENCE: 034536/0323
; CURRENT APPLICATION NUMBER: US/10/618,581
; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: 60/395,624
 ; PRIOR FILING DATE: 2002-07-15
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 994
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-10-618-561-8

Query Match 50.5%; Score 48; DB 15; Length 994;
 Best Local Similarity 72.7%; Pred. No. 89;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDD 16
 DB 277 MLAGYLPFDD 287

RESULT 48
 US-10-080-608A-37
 ; Sequence 37, Application US/10080608A
 ; Publication No. US20030198956A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Makowski, Lee
 ; APPLICANT: Hyman, Paul
 ; APPLICANT: Williams, Mark
 ; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
 ; FILE REFERENCE: 8471-010-999
 ; CURRENT APPLICATION NUMBER: US/10/080,608A
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 1507
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-10-080-608A-37

Query Match 50.5%; Score 48; DB 14; Length 1507;
 Best Local Similarity 64.3%; Pred. No. 1.4e+02;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDDFQL 19
 DB 847 MRAPYIPIDDDMPL 860

RESULT 49
 US-10-370-685-126
 ; Sequence 126, Application US/10370685
 ; Publication No. US20030215903A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyman, Paul
 ; APPLICANT: Goldberg, Edward
 ; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
 ; FILE REFERENCE: NAF P-004
 ; CURRENT APPLICATION NUMBER: US/10/370,685
 ; CURRENT FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: 10/080,608
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 159
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 126
 ; LENGTH: 1507
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-10-370-685-126

Query Match 50.5%; Score 48; DB 15; Length 1507;
 Best Local Similarity 64.3%; Pred. No. 1.4e+02;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDDFQL 19
 DB 847 MRAPYIPIDDDMPL 860

RESULT 50
 US-10-149-823-2
 ; Sequence 2, Application US/10149823
 ; Publication No. US20030152910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stein-Gerlach, Matthias
 ; APPLICANT: Mett, Helmut
 ; APPLICANT: Marschall, Manfred
 ; APPLICANT: Stamming, Thomas
 ; TITLE OF INVENTION: Method for identification and quantification of kinase inhibitors
 ; FILE REFERENCE: AXM-006.0P US
 ; CURRENT APPLICATION NUMBER: US/10/149,823
 ; CURRENT FILING DATE: 2002-06-05
 ; PRIOR APPLICATION NUMBER: EP 99124342.9
 ; PRIOR FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: PCT/EP00/12303
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Human cytomegalovirus
 US-10-149-823-2

Query Match 49.5%; Score 47; DB 14; Length 707;
 Best Local Similarity 41.2%; Pred. No. 86;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDF 17
 DB 304 ELSISYLLVYVPKEDDF 320

Search completed: February 8, 2005, 20:38:02
 Job time : 77.6667 secs

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OM protein - protein search, using sw model

Run on: February 8, 2005, 19:39:04 ; Search time 94.3333 Seconds
(without alignments)
103.140 Million cell updates/sec

Title: US-10-032-361-5

Perfect score: 95
Sequence: 1 DLDLEMLAXYIPMDDDFQL 19

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	766	1 HIFA_ONCMY	Q68w2 oncorhynch
2	95	100.0	774	2 Q6STN7	Q6stn7 ctenopharyn
3	95	100.0	777	2 Q6EH14	Q6eh14 brachydanio
4	95	100.0	786	2 Q6SL11	Q6sl11 canis famil
5	95	100.0	802	2 Q6P154	Q6p154 xenopus lae
6	95	100.0	805	1 HIFA_XENLA	Q6i5a9 xenopus lae
7	95	100.0	811	1 HIFA_CHICK	Q9yib9 gallus gall
8	95	100.0	819	2 Q7YSE5	Q7yse5 oryctolagus
9	95	100.0	821	2 Q64P54	Q64f54 spermophillu
10	95	100.0	823	1 HIFA_BOVIN	Q9xta5 bos taurus
11	95	100.0	823	2 Q6IV47	Q6iv47 bos mutus g
12	95	100.0	824	2 Q6H8T3	Q6h8t3 spalax juda
13	95	100.0	825	1 HIFA_RAT	Q35800 rattus norv
14	95	100.0	826	1 HIFA_HUMAN	Q15665 homo sapien
15	95	100.0	836	1 HIFA_MOUSE	Q61221 mus musculu
16	81	85.3	630	2 Q9X54	Q9qx54 mus musculu
17	81	85.3	632	2 Q8WX1	Q8wxal homo sapien
18	81	85.3	648	2 Q9HAI2	Q9hai2 mus musculu
19	81	85.3	662	2 Q9Z2I5	Q9z2i5 mus musculu
20	81	85.3	667	2 Q9Y2N7	Q9y2n7 homo sapien
21	81	85.3	669	2 Q66K72	Q66k72 homo sapien
22	80	84.2	571	2 Q7T2E4	Q7t2e4 brachydanio
23	80	84.2	626	2 Q6EGR9	Q6egr9 brachydanio
24	80	84.2	643	2 Q6STN6	Q6stn6 ctenopharyn
25	77	81.1	662	2 Q9JHS2	Q9jhs2 rattus norv
26	74.5	78.4	835	2 Q696W2	Q696w2 ctenopharyn
27	74.5	78.4	859	2 Q6GQ12	Q6gq12 xenopus lae
28	74.5	78.4	862	2 Q6GL61	Q6gl61 xenopus tro
29	74.5	78.4	862	2 Q6GP97	Q6gp97 xenopus lae
30	74.5	78.4	873	2 Q8QGM4	Q8qgm4 fundulus he
31	74	77.9	632	2 Q96K34	Q96k34 homo sapien

32	70.5	74.2	163	2	Q6RYD1	Q6ryd1 sus scrofa
33	70.5	74.2	164	2	Q6RYD0	Q6ryd0 ovis aries
34	70.5	74.2	867	2	Q9W7C6	Q9w7c6 gallus gall
35	70.5	74.2	870	1	PAS1_HUMAN	Q99814 homo sapien
36	70.5	74.2	870	2	Q9XTA4	Q9xta4 bos taurus
37	70.5	74.2	870	2	Q9PTB3	Q9ptb3 coturnix co
38	70.5	74.2	874	1	PAS1_MOUSE	Q97481 mus musculu
39	70.5	74.2	874	1	PAS1_RAT	Q97481 rattus norv
40	70.5	74.2	874	2	Q6PEU2	Q6peu2 mus musculu
41	59	62.1	235	2	Q8QGI5	Q8qgi5 fundulus he
42	49	51.6	494	2	Q9AGM7	Q9agm7 legionella
43	48	50.5	339	2	Q8U2M8	Q8u2m8 colletotric
44	48	50.5	492	2	Q7Z993	Q7z993 schizosacch
45	48	50.5	800	1	KIN4_YEAST	Q01919 saccharomyc
46	48	50.5	979	2	Q6BTQ3	Q6btq3 debaryomyce
47	48	50.5	1168	2	Q7SFD3	Q7sfd3 neurospora
48	48	50.5	1507	1	SIMA_DROME	Q24167 drosophila
49	47	49.5	661	2	Q6FPH1	Q6fph1 candida gla
50	47	49.5	688	2	Q7T838	Q7t838 human cytom
51	47	49.5	707	1	GCVK_HCMVA	P16788 human cytom
52	47	49.5	707	2	Q910D5	Q910d5 human cytom
53	47	49.5	707	2	Q910P8	Q910p8 human cytom
54	47	49.5	707	2	Q910W3	Q910w3 human cytom
55	47	49.5	707	2	Q91B46	Q91b46 human cytom
56	47	49.5	707	2	Q91B47	Q91b47 human cytom
57	47	49.5	707	2	Q91B48	Q91b48 human cytom
58	47	49.5	707	2	Q91B49	Q91b49 human cytom
59	47	49.5	707	2	Q91B50	Q91b50 human cytom
60	47	49.5	707	2	Q91B51	Q91b51 human cytom
61	47	49.5	707	2	Q91B52	Q91b52 human cytom
62	47	49.5	707	2	Q91B53	Q91b53 human cytom
63	47	49.5	707	2	Q91B54	Q91b54 human cytom
64	47	49.5	707	2	Q91B55	Q91b55 human cytom
65	47	49.5	707	2	Q68101	Q68101 human cytom

ALIGNMENTS

RESULT 1	HIFA_ONCMY	STANDARD;	PRT;	766 AA.
ID	HIFA_ONCMY	STANDARD;	PRT;	766 AA.
AC	Q98SW2;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).			
GN	Name=HIF1A;			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=21282949; PubMed=11278461; DOI=10.1074/jbc.M009057200;			
RA	Soitamo A.J., Robergh C.M.I., Gassmann M., Sistonen L., Nikimaa M.;			
RT	"Characterization of a hypoxia-inducible factor (HIF-1 alpha) from rainbow trout: accumulation of protein occurs at normal venous oxygen tension."			
RL	J. Biol. Chem. 276:19699-19705(2001).			
CC	-I- FUNCTION: Functions as a master transcriptional regulator of the adaptive response to hypoxia. Binds to core DNA sequence 5'-[AC]CTGG-3' within the hypoxia response element (HRE) of target gene promoters. Activation requires recruitment of transcriptional coactivators (By similarity).			
CC	-I- SUBUNIT: Efficient DNA binding requires heterodimerization of an alpha and a beta/ARNT subunit (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear translocation in response to hypoxia (By similarity).			
CC	-I- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.			
CC	-I- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.			
CC	-I- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.			

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-----
EMBL; AF304864; AAK30364.1; -.
DR HS3P; Q16665; IH2K.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
KW Activator; DNA-binding; Nuclear protein; Repeat;
Transcription regulation.
FT DOMAIN 718 721 Nuclear localization signal (Potential).
FT DNA BIND 17 30 Basic motif.
FT DOMAIN 31 71 Helix-loop-helix motif.
FT DOMAIN 82 159 PAS 1.
FT DOMAIN 230 300 PAS 2.
FT DOMAIN 304 347 PAC.
FT DOMAIN 368 373 Poly-Glu.
SQ SEQUENCE 766 AA; 85049 MW; FC25A4984104DA5B CRC64;

Query Match 100.0%; Score 95; DB 1; Length 766;
Best Local Similarity 94.7%; Pred. No. 2.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 551 DLDLEMLAPYIPMDDDFQL 569

RESULT 2
Q6STN7 PRELIMINARY; PRT; 774 AA.
AC Q6STN7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor-1alpha.
GN Name=hif-1alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY450269; AAR95697.2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; HypoxindfIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 777 AA; 85897 MW; A9AFE2D2732C7A33 CRC64;

Query Match 100.0%; Score 95; DB 2; Length 777;
Best Local Similarity 94.7%; Pred. No. 3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 549 DLDLEMLAPYIPMDDDFQL 567

RESULT 4
Q6SLU1 PRELIMINARY; PRT; 786 AA.
AC Q6SLU1;

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DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 774 AA; 85741 MW; 15BD0B2F90C611C6 CRC64;

Query Match 100.0%; Score 95; DB 2; Length 774;
Best Local Similarity 94.7%; Pred. No. 3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 547 DLDLEMLAPYIPMDDDFQL 565

RESULT 3
Q6EH14 PRELIMINARY; PRT; 777 AA.
AC Q6EH14;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypoxia inducible factor 1 alpha.
GN Name=hif1a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R., Tsai Y.-C., Young H.-W., Wang W.-D., Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY326951; AAG91619.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; HypoxindfIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 777 AA; 85897 MW; A9AFE2D2732C7A33 CRC64;

Query Match 100.0%; Score 95; DB 2; Length 777;
Best Local Similarity 94.7%; Pred. No. 3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
Db 549 DLDLEMLAPYIPMDDDFQL 567

RESULT 4
Q6SLU1 PRELIMINARY; PRT; 786 AA.
AC Q6SLU1;

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DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Hypoxia-inducible factor 1 alpha subunit (Fragment).
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Spee B., Penning L.C., Rothuizen J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY455802; AAR19225.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; HypoxindFIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAC; 2.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
FT NON_TER 1
FT NON_TER 786
SQ SEQUENCE 786 AA; 88015 MW; C37A27C25C343CDC CRC64;

Query Match 100.0%; Score 95; DB 2; Length 786;
Best Local Similarity 94.7%; Pred. No. 3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||:|||||:|||||
Db 536 DLDLEMLAPYIPMDDDFQL 554

RESULT 5
ID Q6PI54 PRELIMINARY; PRT; 802 AA.
AC Q6PI54;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE Hypoxia-inducible factor 1 alpha subunit (Fragment)
DE Hif1a-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC043769; AAH43769.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; HypoxindFIA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAC; 2.
DR PRINTS; PR01080; HYPOXIAFIA.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
DR PROSITE; PS01112; PAS; 2.
SQ SEQUENCE 802 AA; 90177 MW; 30A571277A9A5B1F CRC64;

Query Match 100.0%; Score 95; DB 2; Length 802;
Best Local Similarity 94.7%; Pred. No. 3.1e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFQL 19
|||:|||||:|||||
Db 550 DLDLEMLAPYIPMDDDFQL 568

RESULT 6
HIFA_XENLA
ID HIFA_XENLA STANDARD; PRT; 805 AA.
AC Q918A9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kietzmann T.;
RT "Cloning and expression of the Xenopus laevis hypoxia inducible factor
RT 1 alpha homologue.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Binds to core DNA sequence 5'-

```

CC [AG]CTG-3' within the hypoxia response element (HRE) of target
 CC gene promoters. Activation requires recruitment of transcriptional
 CC coactivators (By similarity).
 CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 CC alpha and a beta/ARNT subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
 CC translocation in response to hypoxia (By similarity).
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
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 CC -----
 CC EMBL; AJ277829; CAB96628.1; -.
 CC HSSP; Q16665; IH2K.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001321; Hypoxindf1A.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR01080; HYPOXIAF1A.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC PROSITE; PS00888; HLH; 1.
 CC PROSITE; PS01112; PAS; 2.
 CC Activator; DNA-binding; Nuclear protein; Repeat;
 KW Transcription regulation.
 FT DNA BIND 17 30 Basic motif.
 FT DOMAIN 31 71 Helix-loop-helix motif.
 FT DOMAIN 85 157 PAS 1.
 FT DOMAIN 229 300 PAS 2.
 FT DOMAIN 303 346 PAC.
 FT SEQUENCE 805 AA; 90964 MW; BABFA0BD6B44FF3B CRC64;
 SQ
 Query Match 100.0%; Score 95; DB 1; Length 805;
 Best Local Similarity 94.7%; Pred. No. 3.1e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 Db 552 DLDLEMLAPYIPMDDDFQL 570
 |||||:|||||
 |||||:|||||
 RESULT 7
 ID HIFA CHICK STANDARD; PRT; 811 AA.
 AC Q9YB9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN Name=HIF1A;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Takahashi T.;
 RT "Molecular cloning and expression of an avian cDNA for hypoxia-
 RT inducible factor-1 alpha in embryonic ventricular myocytes."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions as a master transcriptional regulator of the

CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
 CC [AG]CTG-3' within the hypoxia response element (HRE) of target
 CC gene promoters. Activation requires recruitment of transcriptional
 CC coactivators (By similarity).
 CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 CC alpha and a beta/ARNT subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
 CC translocation in response to hypoxia (By similarity).
 CC -1- DOMAIN: Contains two independent C-terminal transactivation
 CC domains, NTAD and CTAD, which function synergistically. Their
 CC transcriptional activity is repressed by an intervening inhibitory
 CC domain (ID) (By similarity).
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
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 CC -----
 CC EMBL; AB013746; BAA34234.2; -.
 CC HSSP; Q16665; IH2K.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001321; Hypoxindf1A.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR01080; HYPOXIAF1A.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC PROSITE; PS00888; HLH; 1.
 CC PROSITE; PS01112; PAS; 2.
 CC Activator; DNA-binding; Nuclear protein; Repeat;
 KW Transcription regulation.
 FT DNA BIND 17 30 Basic motif.
 FT DOMAIN 31 71 Helix-loop-helix motif.
 FT DOMAIN 80 157 PAS 1.
 FT DOMAIN 228 298 PAS 2.
 FT DOMAIN 302 345 PAC.
 FT DOMAIN 401 587 ODD.
 FT DOMAIN 529 573 NTAD.
 FT DOMAIN 576 785 ID.
 FT DOMAIN 703 706 Nuclear localization signal (Potential).
 FT DOMAIN 718 721 Nuclear localization signal (Potential).
 FT DOMAIN 771 811 CTAD.
 FT DOMAIN 583 588 Poly-Ser.
 FT SEQUENCE 811 AA; 90542 MW; D14CD9FC98F064CB CRC64;
 SQ
 Query Match 100.0%; Score 95; DB 1; Length 811;
 Best Local Similarity 94.7%; Pred. No. 3.1e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFQL 19
 Db 554 DLDLEMLAPYIPMDDDFQL 572
 |||||:|||||
 |||||:|||||
 RESULT 8
 QYSE5
 ID Q7YSE5 PRELIMINARY; PRT; 819 AA.
 AC Q7YSE5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypoxia inducible factor 1 alpha subunit.
 OS Oryctolagus cuniculus (Rabbit).


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DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
KW Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT DOMAIN 718 721
FT DNA_BIND 17 30
FT DOMAIN 31 71
FT DOMAIN 85 158
FT DOMAIN 228 298
FT DOMAIN 302 345
FT DOMAIN 401 600
FT DOMAIN 531 575
FT DOMAIN 576 782
FT DOMAIN 783 823
FT DOMAIN 715 718
FT MOD_RES 90 90
FT MOD_RES 139 139
FT MOD_RES 173 173
FT MOD_RES 194 194
FT MOD_RES 210 210
FT MOD_RES 219 219
FT MOD_RES 224 224
FT MOD_RES 255 255
FT MOD_RES 334 334
FT MOD_RES 337 337
FT MOD_RES 359 359
FT MOD_RES 402 402
FT MOD_RES 520 520
FT MOD_RES 532 532
FT MOD_RES 564 564
FT MOD_RES 755 755
FT MOD_RES 777 777
FT MOD_RES 797 797
FT MOD_RES 800 800
SQ SEQUENCE 823 AA; 92127 MW; 12674E467A61B1A1 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 823;
Best Local Similarity 94.7%; Pred. No. 3.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDLEMLAXYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 11
Q6IV47 PRELIMINARY; PRT; 823 AA.
AC Q6IV47
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia inducible factor-1a.
GN Name=HIF-1a;
OS Bos mutus grunniens (Yak).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=30521;
RN [1]
RP SEQUENCE FROM N.A.
RA Dolt K.S., Qadar Pasha M.A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

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DR EMBL; AY621118; AAT39520.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 823 AA; 92128 MW; A6E388E4FEA15705 CRC64;

Query Match 100.0%; Score 95; DB 2; Length 823;
Best Local Similarity 94.7%; Pred. No. 3.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDLEMLAXYIPMDDDFQL 19
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 12
Q6H8T3 PRELIMINARY; PRT; 824 AA.
AC Q6H8T3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia inducible factor 1 alpha.
GN Name=hif-1a;
OS Spalax judaei (Blind subterranean mole rat).
OC Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC Spalax.
OX NCBI_TaxID=134510;
RN [1]
RP SEQUENCE FROM N.A.
RA Shams I., Aviari A., Nevo E.;
RL "Hypoxic stress tolerance of the subterranean mole rat: Expression of erythropoietin and hypoxia-inducible factor-1a.";
RL Nucleic Acids Res. 0:0-0(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=15210955; DOI=10.1073/pnas.0403540101;
RA Shams I., Aviari A., Eviatar N.;
RL "Hypoxic stress tolerance of the blind subterranean mole rat: expression of erythropoietin and hypoxia-inducible factor 1 alpha.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9698-9703(2004).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AJ715791; CAG29396.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.

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DR PRINTS; PRO1080; HYPOXIAIF1A.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS00888; HLH; 1.
 DR PROSITE; PS0112; PAS; 2.
 SQ SEQUENCE 824 AA; 92161 MW; 33A1DDC3593CBFF CRC64;
 Query Match 100.0%; Score 95; DB 2; Length 824;
 Best Local Similarity 94.7%; Pred. No. 3.2e-06;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDLEMLAXYIPMDDDFOL 19
 DB 556 DLDLEMLAXYIPMDDDFOL 574
 RESULT 13
 HIPA RAT
 ID HIFA RAT STANDARD; PRT; 825 AA.
 AC O35800; Q9WTU9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (Hif-1 alpha) (HIF1 alpha).
 GN Name=Hif1a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Hepatocytes;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
 RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perivenous expression of the mRNA of the three hypoxia-inducible
 factor a-subunits Hif-1a, Hif2a and Hif3a in rat liver.";
 RL Biochem. J. 354:531-539(2001).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=21417706; PubMed=11526200;
 RA Zou A.-P., Yang Z.-Z., Li P.-L., Cowley A.W. Jr.;
 RT "Oxygen-dependent expression of hypoxia-inducible factor-1alpha in
 renal medullary cells of rats.";
 RL Physiol. Genomics 6:159-168(2001).
 CC -!- FUNCTION: Functions as a master transcriptional regulator of the
 CC adaptive response to hypoxia. Under hypoxic conditions activates
 CC the transcription of over 40 genes, including, erythropoietin,
 CC glucose transporters, glycolytic enzymes, vascular endothelial
 CC growth factor, and other genes whose protein products increase
 CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
 CC Plays an essential role in embryonic vascularization, tumor
 CC angiogenesis and pathophysiology of ischemic disease. Binds to
 CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
 CC element (HRE) of target gene promoters. Activation requires
 CC recruitment of transcriptional coactivators such as CREBBP and
 CC EP300. Activity is enhanced by interaction with both, NCOA1 or
 CC NCOA2. Interaction with redox regulatory protein APEX seems to
 CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
 CC similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 CC alpha and a beta/ARNT subunit. Binds to the TA2-type 1 domains of
 CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APX and HSP90 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
 CC translocation in response to hypoxia (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is
 CC seen in the renal medulla than in the cortex. Expressed also in
 CC the perivenous zone of the liver.
 CC -!- DOMAIN: Contains two independent C-terminal transactivation
 CC domains, NTAD and CTAD, which function synergistically. Their
 CC transcriptional activity is repressed by an intervening inhibitory
 CC domain (ID) (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the
 CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
 CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563.
 CC The hydroxylated prolines promote interaction with VHL, initiating
 CC rapid ubiquitination and subsequent proteasomal degradation. Under
 CC hypoxia, proline hydroxylation is impaired and ubiquitination is
 CC attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus
 CC abrogating interaction with CREBBP and EP300 and preventing
 CC transcriptional activation (By similarity).
 CC -!- PTM: S-nitrosylated. All free thiol groups are subjected to S-
 CC nitrosylation in vitro, however not all thiol groups seem to be
 CC nitrosylated in vivo (By similarity).
 CC -!- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL
 CC and stimulates subsequent proteasomal degradation (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; Y09507; CAA70701.1; -.
 CC EMBL; AF057308; AAD24413.1; -.
 CC HSSP; Q16665; 1L8C.
 CC TRANSFAC; T05461; -.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001321; Hypoxindf1A.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR01080; HYPOXIAIF1A.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC PROSITE; PS00888; HLH; 1.
 CC PROSITE; PS0112; PAS; 2.
 KW Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
 KW Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
 FT DOMAIN 718 721 Nuclear localization signal (Potential).
 FT DNA_BIND 17 30 Helix-loop-helix motif.
 FT DOMAIN 31 71 Basic motif.
 FT DOMAIN 85 158 PAS 1.
 FT DOMAIN 228 298 PAS 2.
 FT DOMAIN 302 345 PAC.
 FT DOMAIN 401 602 ODD.
 FT DOMAIN 530 574 NTAD.
 FT DOMAIN 575 784 ID.
 FT DOMAIN 717 720 Nuclear localization signal (Potential).
 FT DOMAIN 785 825 CTAD.
 FT MOD_RES 90 90 S-nitrosocysteine (Potential).
 FT MOD_RES 139 139 S-nitrosocysteine (Potential).
 FT MOD_RES 173 173 S-nitrosocysteine (Potential).
 FT MOD_RES 194 194 S-nitrosocysteine (Potential).
 FT MOD_RES 210 210 S-nitrosocysteine (Potential).
 FT MOD_RES 219 219 S-nitrosocysteine (Potential).
 FT MOD_RES 224 224 S-nitrosocysteine (Potential).
 FT MOD_RES 255 255 S-nitrosocysteine (Potential).
 FT MOD_RES 334 334 S-nitrosocysteine (Potential).
 FT MOD_RES 337 337 S-nitrosocysteine (Potential).
 FT MOD_RES 385 385 S-nitrosocysteine (Potential).
 FT MOD_RES 402 402 Hydroxyproline (By similarity).
 FT MOD_RES 519 519 S-nitrosocysteine (Potential).
 FT MOD_RES 531 531 N6-acetyllysine (By similarity).

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FT MOD_RES 563 Hydroxyproline (By similarity).
FT MOD_RES 779 S-nitrosocysteine (Potential).
FT MOD_RES 799 S-nitrosocysteine (Potential).
FT MOD_RES 802 3-hydroxyasparagine (By similarity).
FT CONFLICT 12 K -> NR (in Ref. 2).
FT CONFLICT 74 D -> G (in Ref. 2).
FT CONFLICT 96 P -> L (in Ref. 2).
FT CONFLICT 329 D -> N (in Ref. 2).
FT CONFLICT 613 ATATTAT -> TATA (in Ref. 2).
FT CONFLICT 708 ATATTAT -> K (in Ref. 2).
SQ SEQUENCE 825 AA; 92319 MW; C4109A57F38667E9 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 825;
Best Local Similarity 94.7%; Pred. No. 3.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDFOL 19
Db 555 DLDLEMLAPYIPMDDDFOL 573

RESULT 14
HIFA HUMAN
ID HIFA HUMAN STANDARD; PRT; 826 AA.
AC Q16655; O96P79; Q9UPB1;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 25-OCT-2004 (Rel. 45; Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE interacting protein) (Member of PAS protein 1) (MOP1).
GN Name=HIF1A;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1] _SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
RX MEDLINE=95296340; PubMed=7539918;
RA Wang G.L., Jiang B.H., Rue E.A., Semenza G.L.;
RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
RT heterodimer regulated by cellular O2 tension.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatoma;
RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS
RT superfamily that interacts with components of the dioxin signaling
RT pathway.";
RL J. Biol. Chem. 272:8581-8593(1997).
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99000835; PubMed=9782081; DOI=10.1006/geno.1998.5416;
RA Iyer N.V., Leung S.W., Semenza G.L.;
RT "The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
RT evolutionary conservation.";
RL Genomics 52:159-165(1998).
[4]
RP SEQUENCE FROM N.A.
RA Rupert J.L., Hochachka P.W.;
RT "HIF1a sequence in the Quechua, a high altitude population.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Glioblastoma;
RA Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Liver;
RA Tanaka S., Sugimachi K.;

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RT "Hypoxia-inducible factor-1 alpha variant isolated from human liver
RT tissue.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Choriocarcinoma, and Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RN TRANSACTIVATION DOMAINS NTD AND CTAD.
RX MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;
RA Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;
RT "Transactivation and inhibitory domains of hypoxia-inducible factor
RT 1alpha. Modulation of transcriptional activity by oxygen tension.";
RL J. Biol. Chem. 272:19253-19260(1997).
[9]
RN SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.
RX MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;
RA Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,
RA Poellinger L.;
RT "Signal transduction in hypoxic cells: inducible nuclear translocation
RT and recruitment of the CBP/p300 coactivator by the hypoxia-inducible
RT factor-1alpha.";
RL EMBO J. 17:6573-6586(1998).
[10]
RN OXYGEN-DEPENDENT DEGRADATION DOMAIN.
RX MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;
RA Huang L.E., Gu J., Schau M., Bunn H.F.;
RT "Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-
RT dependent degradation domain via the ubiquitin-proteasome pathway.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992(1998).
[11]
RN TRANSACTIVATION DOMAINS NTD AND CTAD, INTERACTION WITH APEX, AND
RN MUTAGENESIS OF CYS-800.
RX MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA Poellinger L., Fujii-Kuriyama Y.;
RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT in response to hypoxia: their stabilization and redox signal-induced
RT interaction with CBP/p300.";
RL EMBO J. 18:1905-1914(1999).
[12]
RN INTERACTION WITH NCOAL1, NCOA2 AND APEX.
RX MEDLINE=20063199; PubMed=10594042;
RA Carrero P., Okamoto K., Coumalleau P., O'Brien S., Tanaka H.,
RA Poellinger L.;
RT "Redox-regulated recruitment of the transcriptional coactivators CREB-
RT binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";
RL Mol. Cell. Biol. 20:402-415(2000).
[13]
RN MUTAGENESIS OF SER-551 AND THR-552.
RX MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;
RA Sutter C.H., Laughner E., Semenza G.L.;
RT "Hypoxia-inducible factor 1alpha protein expression is controlled by

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RT oxygen-regulated ubiquitination that is disrupted by deletions and
RT missense mutations.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753(2000).
RN [14]
RP UBIQUITINATION.
RX MEDLINE=21214630; PubMed=1292861; DOI=10.1126/science.1059796;
RA Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
RA Gaskell S.J., von Kriegsheim A., Hebestreit H.F., Mukherji M.,
RA Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.;
RT "Targeting of HIF-1alpha to the von Hippel-Lindau ubiquitylation
RT complex by O2-regulated prolyl hydroxylation.";
RL Science 292:468-472(2001).
RN [15]
RP S-NITROSYLATION.
RX MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793(02)03887-5;
RA Sumbayev V.V., Budde A., Zhou J., Bruene B.;
RT "HIF-1 alpha protein as a target for S-nitrosation.";
RL FEBS Lett. 535:106-112(2003).
RN [16]
RP ACETYLATION OF LYS-532.
RX MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674(02)01085-1;
RA Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
RA Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
RT "Regulation and destabilization of HIF-1alpha by ARD1-mediated
RT acetylation.";
RL Cell 111:709-720(2002).
RN [17]
RP HYDROXYLATION OF ASN-803.
RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA Bruck R.K.;
RT "Fih-1 is an asparaginyl hydroxylase enzyme that regulates the
RT transcriptional activity of hypoxia-inducible factor.";
RL Genes Dev. 16:1466-1471(2002).
RN [18]
RP HYDROXYLATION OF PRO-402 AND PRO-564.
RX MEDLINE=21558930; PubMed=11598268; DOI=10.1126/science.1066373;
RA Bruck R.K., McKnight S.L.;
RT "A conserved family of prolyl-4-hydroxylases that modify HIF.";
RL Science 294:1337-1340(2001).
RN [19]
RP REVIEW.
RX MEDLINE=20407247; PubMed=10950862;
RA Semenza G.L.;
RT "HIF-1 and human disease: one highly involved factor.";
RL Genes Dev. 14:1983-1991(2000).
RN [20]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=20539371; PubMed=11089639;
RA Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
RA Michiels C.;
RT "A model for the complex between the hypoxia-inducible factor-1 (HIF-
RT 1) and its consensus DNA sequence";
RL J. Biomol. Struct. Dyn. 18:169-179(2000).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
RP HIF1AN.
RX MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
RA Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.F.,
RA Schlemminger I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
RT "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
RT mechanism of oxidative modification of HIF-1 alpha.";
RL J. Biol. Chem. 278:1802-1806(2003).
RN [22]
RP STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
RX MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
RA Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
RA Wagner G., Eck M.J.;
RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
RT factor-1 alpha.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372(2002).
RN [23]
RP STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.

RX MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
RA Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
RA Wright P.E.;
RT "Structural basis for Hif-1 alpha /CBP recognition in the cellular
RT

Query Match 100.0%; Score 95; DB 1; Length 826;
Best Local Similarity 94.7%; Pred. No. 3.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDDFQL 19
|||||:|||||
DB 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 15
HIFA_MOUSE
ID HIFA_MOUSE -STANDARD; PRT: 836 AA
AC Q61221; O08741; O08993; Q61664; Q61665; Q8C681; Q8CC19; Q8CCB6;
AC Q8R385; Q9CYA8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (ARNT
DE interacting protein).
GN Name=Hif1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Hepatocytes;
RX MEDLINE=96355491; PubMed=8702901; DOI=10.1074/jbc.271.35.21262;
RA Li H., Ko H.P., Whitlock J.P. Jr.;
RT "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
RT Roles of Arnt and Hif1alpha.";
RL J. Biol. Chem. 271:21262-21267(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=129/SVJ;
RX MEDLINE=98034461; PubMed=9368100;
RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
RA Bradfield C.A.;
RT "Molecular characterization of the murine Hif-1 alpha locus.";
RL Gene Expr. 6:287-299(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=129/SVJ;
RX MEDLINE=97354184; PubMed=9210478;
RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
RA Gassmann M.;
RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
RT organization, expression and characterization of an alternative first
RT exon and 5' flanking sequence.";
RL Eur. J. Biochem. 246:155-165(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Colon, Diaphragm, Embryo, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maitais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 13-822 FROM N.A. (ISOFORM 2).
RC TISSUE=Hepatocytes;
RX MEDLINE=96254028; PubMed=8660378; DOI=10.1006/bbr.1996.0845;
RA Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.;
RT "Nucleotide sequence, chromosomal assignment and mRNA expression of
mouse hypoxia-inducible factor-1 alpha";
RL Biochem. Biophys. Res. Commun. 223:54-59(1996).
RN [7]
RP SEQUENCE OF 22-85 FROM N.A.
RC TISSUE=Hepatocytes;
RA O'Rourke J.F.;
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a master transcriptional regulator of the
adaptive response to hypoxia. Under hypoxic conditions activates
the transcription of over 40 genes, including, erythropoietin,
glucose transporters, glycolytic enzymes, vascular endothelial
growth factor, and other genes whose protein products increase
oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
angiogenesis and pathophysiology of ischemic disease. Binds to
core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
element (HRE) of target gene promoters. Activation requires
recruitment of transcriptional coactivators such as CREBBP and
EP300. Activity is enhanced by interaction with both, NCOA1 or
NCOA2. Interaction with redox regulatory protein APEX seems to
activate CTAD and potentiates activation by NCOA1 and CREBBP (By
similarity).
CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
alpha and a beta/ARNT subunit. Binds to the TA2-type 1 domains of
CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
translocation in response to hypoxia (By similarity).
CC

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q61221-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q61221-2; Sequence=VSP_007739;
CC TISSUE SPECIFICITY: Ubiquitous.
CC -1- DOMAIN: Contains two independent C-terminal transactivation
domains, NTAD and CTAD, which function synergistically. Their
transcriptional activity is repressed by an intervening inhibitory
domain (ID) (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-577 in the
oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-577.
CC The hydroxylated prolines promote interaction with VHL, initiating
rapid ubiquitination and subsequent proteasomal degradation. Under
hypoxia, proline hydroxylation is impaired and ubiquitination is
attenuated, resulting in stabilization (By similarity).
CC -1- PTM: In normoxia, is hydroxylated on Asn-813 by HIF1AN, thus
abrogating interaction with CREBBP and EP300 and preventing
transcriptional activation (By similarity).
CC -1- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
nitrosylation in vitro, however not all thiol groups seem to be
nitrosylated in vivo (By similarity).
CC -1- PTM: Acetylation of Lys-545 by ARD1 increases interaction with VHL
and stimulates subsequent proteasomal degradation (By similarity).
CC -1- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U59496; AAC52730.1; -;
CC EMBL; AF003695; AAC53455.1; -;
CC EMBL; Y09085; CAA70306.1; JOINED.
CC EMBL; Y13656; CAA70306.1; JOINED.
CC EMBL; Y09085; CAA70305.1; -;
CC EMBL; AF004155; AAC53461.1; JOINED.
CC EMBL; AF004141; AAC53461.1; JOINED.
CC EMBL; AF004142; AAC53461.1; JOINED.
CC EMBL; AF004143; AAC53461.1; JOINED.
CC EMBL; AF004144; AAC53461.1; JOINED.
CC EMBL; AF004145; AAC53461.1; JOINED.
CC EMBL; AF004146; AAC53461.1; JOINED.
CC EMBL; AF004147; AAC53461.1; JOINED.
CC EMBL; AF004148; AAC53461.1; JOINED.
CC EMBL; AF004149; AAC53461.1; JOINED.
CC EMBL; AF004150; AAC53461.1; JOINED.
CC EMBL; AF004151; AAC53461.1; JOINED.
CC EMBL; AF004152; AAC53461.1; JOINED.
CC EMBL; AF004153; AAC53461.1; JOINED.
CC EMBL; AF004154; AAC53461.1; JOINED.
CC EMBL; AF004087; BAC28578.1; -;
CC EMBL; AK034077; BAC36320.1; -;
CC EMBL; AK076395; BAC36320.1; -;
CC EMBL; AK033471; BAC28305.1; -;
CC EMBL; AK017853; BAC30975.1; -;
CC EMBL; BC026139; AAH26139.1; -;
CC EMBL; X95580; CAA64833.1; -;
CC EMBL; X95002; CAA64458.1; -;
CC PIR; JC4837; JC4837.
CC TRANSFAC; T04666; -;
CC MGD; MGI:106918; Hif1a.
CC GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.
CC GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.

Query Match 100.0%; Score 95; DB 1; Length 836;
Best Local Similarity 94.7%; Pred. No. 3.2e-06;

RESULT 20

ID	Q9Y2N7	PRELIMINARY;	PRT;	667 AA.
AC	Q9Y2N7;			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DC	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Putative homolog of hypoxia inducible factor three alpha (Hypoxia-inducible factor-3 alpha).			
GN	Name=HIF-3A;			
OS	Homo sapiens	(Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI TaxID=9606;			

[1] SEQUENCE FROM N.A.
RP Lamerdin J.E., McCready P.M., Skowronski E., Viewanathan V.,
RA Burkhardt-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krombly B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
PL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.

Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
Dangann L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
Submitted (APR-1999) to the EMBL/genBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RP

RA	Olsen A.S., Carrano A.V.;
RB	Submitted (APR-1999) to the ENBL/GenBank/DBDJ databases.
RC	[2]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Kidney;
RR	MEDLINE=21458377; PubMed=11573933; DOI=10.1006/bbrc.2001.5659;
RX	Hara S., Hamada J., Kobayashi C., Kondo Y., Imura N.;
RY	"Expression and characterization of hypoxia-inducible factor (HIF)-
RT	alpha in human kidney: suppression of HIF-mediated gene expression by
RT	HIF-3alpha.";
RT	RT
RL	Biochem. Biophys. Res. Commun. 287:808-813 (2001).
CC	- I- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR	ENBL; AC007193; RAD22668.1; -.
DR	ENBL; AB054067; BAB69689.1; -.
DR	PIR; JC7771; JC7771.
DR	HSP; Q16665; 1LOB.
DR	Genew; HGNC:15825; HIF3A.
DR	GO; GO:005634; C:nucleus; IEA.
DR	GO; GO:0004871; F:signal transducer activity; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	InterPro; IPR001092; HLH_basic.
DR	InterPro; IPR001067; Nuc.translocat.
DR	InterPro; IPR001610; PAC.
DR	InterPro; IPR000014; PAS.
DR	Pfam; PF00010; HLH; 1.
DR	Pfam; PF00989; PAS; 1.
DR	PRINTS; PR00785; NCTRNS.LOCATR.
DR	SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS0112; PAS; 2.
SQ SEQUENCE 667 AA; 72404 MW; 67B8794FF9DCCF4B CRC64;

Query Match 85.3%; Score 81; DB 2; Length 667;
Best Local Similarity 88.9%; Pred. No. 0.00044;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLEMLAXYIPMDDDFQL 19
|||||:|||||
DB 483 LDLEMLAPIISMDDDFQL 500

RESULT 21

Q66K72 PRELIMINARY; PRT; 669 AA.
AC Q66K72;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE HIFA protein.
GN Name=HIF3A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
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RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshikiyuki S., Carninci P., Prange C.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

Query Match 85.3%; Score 81; DB 2; Length 669;
Best Local Similarity 88.9%; Pred. No. 0.00044;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDLEMLAXYIPMDDDFQL 19

DB 485 LDLEMLAPIISMDDDFQL 502
|||||:|||||
QY 1 LDLEMLAXYIPMDDDFQL 19

RESULT 22

Q7T2E4 PRELIMINARY; PRT; 571 AA.
AC Q7T2E4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein hif1a1.
GN Name=hif1a1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Strausberg R.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC054582; AAH54582.1; -

DR HSSP; Q99814; 1P97.

DR ZFIN; ZDB-GENE-040426-1315; hif1a1.

DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR001610; PAS.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAS; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS0112; PAS; 2.

KW Hypothetical protein.

SQ SEQUENCE 571 AA; 63846 MW; 1BA8E4ACC29F16672 CRC64;

Query Match

Best Local Similarity 84.2%; Score 80; DB 2; Length 571;

Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDLEMLAXYIPMDDDFQL 19

DB 430 LDLEMLAPIISMDDDFQL 448

RESULT 23

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Q6EGR9
ID Q6EGR9 PRELIMINARY; PRT; 626 AA.
AC Q6EGR9;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hif3a.
GN Name=hif3a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-R.; Hu C.-H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY330295; AAQ94179.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 626 AA; 70221 MW; EA12390DFECF90B9 CRC64;

Query Match 84.2%; Score 80; DB 2; Length 626;
Best Local Similarity 78.9%; Pred. No. 0.00059;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAXIIPMDDDFQL 19
:||||:||||:|||||
Db 485 ELDLMLAPYISMDDDFQL 503

RESULT 24
Q6STN6 PRELIMINARY; PRT; 643 AA.
AC Q6STN6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypoxia-inducible factor-4alpha.
GN Name=hif-4alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W.; Wu R.S.S.; Mok H.O.L.; Yu R.M.K.; Ng P.K.S.; Kong R.Y.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450270; AAR95698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00989; PAS; 1.

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DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 643 AA; 72434 MW; D73C6DDDD10086C4D CRC64;

Query Match 84.2%; Score 80; DB 2; Length 643;
Best Local Similarity 78.9%; Pred. No. 0.00061;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLDLEMLAXIIPMDDDFQL 19
:||||:||||:|||||
Db 495 ELDLMLAPYISMDDDFQL 513

RESULT 25
Q9JHS2 PRELIMINARY; PRT; 662 AA.
ID Q9JHS2;
AC Q9JHS2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypoxia inducible factor 3 alpha.
GN Name=hif-3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
RA Kietzmann T., Cornesse Y., Brechtel K., Modarresi S., Jungermann K.;
RT "Periveneous expression of the mRNA of the three hypoxia-inducible
factor a-subunits Hif-1a, Hif2a and Hif3a in rat liver.";
RL Biochem. J. 354:531-537(2001).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AJ277827; CAB96611.1; -.
DR HSSP; Q99814; 1997.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00989; PAS; 1.
DR PRINTS; PR00785; NCTRNSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 662 AA; 72887 MW; AC9672E340544010 CRC64;

Query Match 81.1%; Score 77; DB 2; Length 662;
Best Local Similarity 88.2%; Pred. No. 0.0019;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DLEMLAXIIPMDDDFQL 19
|||||:|||||
Db 481 DLEMLAPYISMDDDFQL 497

RESULT 26
Q696W2 PRELIMINARY; PRT; 835 AA.
ID Q696W2;
AC Q696W2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

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DE Hypoxia-inducible factor 2 alpha.
GN Name=hif-2alpha;
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RA Law S.H.W., Kong R.Y.C., Wu R.S.S.;
RT "Molecular characterization of hypoxia-inducible factor-2alpha (hif-2alpha) gene in grass carp."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY577524; AAT76668.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:regulation of transcription; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTNRSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 835 AA; 92830 MW; CAE59B9AFC785FD CRC64;

Query Match 78.4%; Score 74.5; DB 2; Length 835;
Best Local Similarity 80.0%; Pred. No. 0.006;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAXYIPMD-DDFQL 19
|||||:|||||:|||||
Db 518 DLDLETLAPYIPMDGEDFQL 537

RESULT 27
Q6GQ12 PRELIMINARY; PRT; 859 AA.
AC Q6GQ12;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE MGC80468 protein.
GN Name=MGC80468;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schain J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC072936; AAH72936.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR00785; NCTNRSLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 859 AA; 96956 MW; 59D477E1929A0AD6 CRC64;

Query Match 78.4%; Score 74.5; DB 2; Length 859;
Best Local Similarity 80.0%; Pred. No. 0.0062;
Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DLDLEMLAXYIPMD-DDFQL 19
|||||:|||||:|||||
Db 517 DLDLETLAPYIPMDGEDFQL 536

RESULT 28
Q6GL61 PRELIMINARY; PRT; 862 AA.
AC Q6GL61;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Epas1-prov protein.
GN Name=epas1-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL; BC073244; AAH73244.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR DR GO; GO:0007165; P:signal transduction; IEA.
 DR DR InterPro; IPR001092; HLH basic.
 DR DR InterPro; IPR001067; Nuc translocat.
 DR DR InterPro; IPR001610; PAC.
 DR DR InterPro; IPR000014; PAC.
 DR DR Pfam; PF00010; HLH; 1.
 DR DR Pfam; PF00785; PAC; 1.
 DR DR Pfam; PF00989; PAC; 1.
 DR DR PRINTS; PR00785; NCTNLSLOCAT.
 DR DR SMART; SM00353; HLH; 1.
 DR DR SMART; SM00086; PAC; 1.
 DR DR SMART; SM00091; PAC; 2.
 DR DR PROSITE; PS00888; HLH; 1.
 DR DR PROSITE; PS0112; PAC; 2.
 DR DR PROSITE; PS0112; PAC; 2.
 SQ SEQUENCE 862 AA; 97319 MW; 3AC8FB3932E9E60 CRC64;

 Query Match 78.4%; Score 74.5; DB 2; Length 862;
 Best Local Similarity 80.0%; Pred. No. 0.0062;
 Matches 16; Conservative 2; Mismatches 1; Indels 1; Gaps

 Qy 1 LDLEMLAXYIPMD-DDFQL 19
 |||||:||||:||||
 Db 518 LDLETLAPYIPMDGEDPQL 537

 RESULT 30
 Q8QGM4 ID Q8QGM4 PRELIMINARY; PRT; 873 AA.
 AC Q8QGM4;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypoxia-inducible factor 2 alpha.
 OS Fundulus heteroclitus (Killifish) (Mummichog).

Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musakawa K., Yuuki H., Oshima A., Saeki N., Aotsuka S., Yoshikino Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togaashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Maehuo Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human cDNAs.";

RL Nat. Genet. 36:40-45(2004).

CC -I- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AK027725; BAB55324.1; --

DR HSSP; Q9814; 1P97.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004871; P:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPRO01092; HLH_basic.

DR InterPro; IPRO01067; Nuc_translocat.

DR InterPro; IPRO01610; PAC.

DR InterPro; IPRO00014; PAS.

DR Pfam; PF00989; PAS; 1.

DR PRINTS; PR00785; NCTRNSLOCATF.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS50112; PAS; 2.

SQ SEQUENCE 632 AA; 66933 MW; A19FIED3D05E7A71 CRC64;

Query Match 77.9%; Score 74; DB 2; Length 632;
Best Local Similarity 83.3%; Pred.No. 0.0054;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LDLEMLAXYIPMDDFQL 19
|||||:|:|:|:|:|
Db 485 LDLEMLAPYISMGGDFQL 502

RESULT 32

Q6RYD1 PRELIMINARY; PRT; 163 AA.

ID Q6RYD1

AC Q6RYD1;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Endothelial PAS domain protein 1 (Fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC NCBI_Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

RN NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Ing N.H., Balog C.J., Wolfskill R.L.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY485673; AAR37390.1; --

FT NON_TER 1

FT FT 163

SQ SEQUENCE 163 AA; 17207 MW; 679CDA9F183CCAD3 CRC64;

Query Match 74.2%; Score 70.5; DB 2; Length 163;


```

Best Local Similarity 75.0%; Pred. No. 0.0048;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAXYIPMD-DDFOL 19
Db 118 ELDELTAPYIPMDGEDFOL 137

RESULT 33
Q6RYD0
ID Q6RYD0 PRELIMINARY; PRT; 164 AA.
AC Q6RYD0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Endothelial PAS domain protein 1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
ON NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Ing N.H., Balog C.J., Wolfskill R.L.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485674; AAR37391.1; -.
FT NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 17405 MW; 49DBB95BA3D6D826 CRC64;

Query Match 74.2%; Score 70.5; DB 2; Length 164;
Best Local Similarity 75.0%; Pred. No. 0.0048;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAXYIPMD-DDFOL 19
Db 119 ELDELTAPYIPMDGEDFOL 138

RESULT 34
Q9W7C6
ID Q9W7C6 PRELIMINARY; PRT; 867 AA.
AC Q9W7C6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endothelial PAS domain protein 1.
GN Name=EPAS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-bred White Leghorn;
RX MEDLINE=20047819; PubMed=10580084; DOI=10.1016/S0014-5793(99)01476-3;
RA Pavier J., Kempf H., Corvol P., Gasc J.-M.;
RT "Cloning and expression pattern of EPAS1 in the chicken embryo.
RT Colocalization with tyrosine hydroxylase."
RL FEBS Lett. 462:19-24(1999).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AF129813; AAD38358.1; -.
DR HSSP; Q99814; 1P97.
DR GO; GO:0005633; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001067; Nuc_translocat.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.

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Pfam; PF00010; HLH; 1.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 1.
PRINTS; PR00785; NCTRNLOCATR.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 867 AA; 97133 MW; DE674A948DE11DCC CRC64;

Query Match 74.2%; Score 70.5; DB 2; Length 867;
Best Local Similarity 75.0%; Pred. No. 0.027;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAXYIPMD-DDFOL 19
Db 522 ELDELTAPYIPMDGEDFOL 541

RESULT 35
PASI_HUMAN
ID PASI_HUMAN STANDARD; PRT; 870 AA.
AC Q99814; Q86VA2; Q99630;
DT 15-DEC-1998 (Rel. 37, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2)
DE (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha)
DE (HIF-1 alpha-like factor) (HLF).
GN Name=EPAS1; Synonyms=HIF2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152468; PubMed=9000051;
RA Tian H., McKnight S.L., Russell D.W.;
RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT selectively expressed in endothelial cells."
RL Genes Dev. 11:72-82(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Hepaticoma;
MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA Pray-Grant M., Perdev G.H., Bradfield C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS
RT superfamily that interacts with components of the dioxin signaling
RT pathway."
RL J. Biol. Chem. 272:8581-8593(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Eye;
MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[4]
TRANSCRIPTION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
MUTAGENESIS OF CYS-844.
MEDLINE-99219869; PubMed-10202154; DOI=10.1093/emboj/18.7.1905;
Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
Poellinger L., Fujii-Kuriyama Y.;
"Molecular mechanisms of transcription activation by HLF and HIF1alpha
in response to hypoxia: their stabilization and redox signal-induced
interaction with CBP/p300.";
EMBO J. 18:1905-1914 (1999).
CC -!- FUNCTION: Transcription factor involved in the induction of oxygen
regulated genes. Binds to core DNA sequence 5'-(AG)CTGG-3' within
the hypoxia response element (HRE) of target gene promoters.
CC Regulates the vascular endothelial growth factor (VEGF) expression
and seems to be implicated in the development of blood vessels and
the tubular system of lung. May also play a role in the formation
of the endothelium that gives rise to the blood brain barrier.
CC Potent activator of the Tie-2 tyrosine kinase expression.
CC Activation seems to require recruitment of transcriptional
coactivators such as CREBBP and probably EP300. Interaction with
redox regulatory protein APEX seems to activate CTAD.
CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP (By
similarity).
CC -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
in placenta, lung and heart. Selectively expressed in endothelial
cells.
CC -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-531
by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
prolines promote interaction with VHL, initiating rapid
ubiquitination and subsequent proteasomal degradation. Under
hypoxia, proline hydroxylation is impaired and ubiquitination is
attenuated, resulting in stabilization (By similarity).
CC -!- PTM: In normoxia, is hydroxylated on Asn-847 by HIF1AN thus
probably abrogating interaction with CREBBP and EP300 and
preventing transcriptional activation (By similarity).
CC -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; U81984; AB941495.1; -;
CC EMBL; U51626; AAC51212.1; -;
CC EMBL; BC051338; AAH51338.1; -;
CC PDB; 1P97; NMR; A=237-350.
CC TRANSFAC; T02718; -;
CC Genew; HGNC:3374; EPAS1.
CC MIM; 603349; -;
CC GO; GO:0003705; P:RNA polymerase II transcription factor acti. . . ; TAS..
CC GO; GO:0003713; P:transcription coactivator activity; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC GO; GO:0006366; P:transcription from Pol II promoter; TAS.
CC InterPro; IPR001092; HLH basic.
CC InterPro; IPR001067; NUC translocat.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS.
CC Pfam; PF00010; HLH; 1.
CC Pfam; PF00785; PAC; 1.
CC Pfam; PF00989; PAS; 1.
CC PRINTS; PR00785; NCTNSLOCATR.
CC SMART; SM00353; HLH; 1.
CC SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
KW 3D-structure; Activator; Angiogenesis; Developmental protein;
KW DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW Transcription regulation.
FT DNA_BIND 15 27 Basic motif.
FT DOMAIN 28 68 Helix-loop-helix motif.
FT DOMAIN 84 154 PAS 1.
FT DOMAIN 230 300 PAS 2.
FT DOMAIN 304 347 PAC.
FT DOMAIN 496 542 NTAD.
FT DOMAIN 830 870 CTAD.
FT DOMAIN 474 480 Poly-Ser.
FT MOD_RES 405 405 Hydroxyproline (By similarity).
FT MOD_RES 531 531 Hydroxyproline (By similarity).
FT MOD_RES 840 840 Phosphothreonine (By similarity).
FT MOD_RES 847 847 3-hydroxyasparagine (By similarity).
FT MUTAGEN 844 844 C->S: Abolishes hypoxia-inducible
transcriptional activation of ctad.
FT CONFLICT 60 60 A -> E (in Ref. 1).
FT CONFLICT 539 539 D -> G (in Ref. 2).
FT CONFLICT 601 601 H -> R (in Ref. 2).
FT CONFLICT 693 693 D -> N (in Ref. 2).
FT CONFLICT 716 716 E -> K (in Ref. 2).
FT CONFLICT 722 722 L -> P (in Ref. 2).
FT CONFLICT 765 765 F -> L (in Ref. 2).
FT CONFLICT 769 769 P -> S (in Ref. 2).
FT CONFLICT 844 844 C -> R (in Ref. 2).
FT CONFLICT 847 847 N -> K (in Ref. 2).
SQ SEQUENCE 870 AA; 96458 MW; 4838989598234FC1 CRC64;
Query Match 74.2%; Score 70.5; DB 1; Length 870;
Best Local Similarity 75.0%; Pred. No. 0.027;
Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 DLDLEMLAXYIPMD-DDFQL 19
:|||||:|||||:|||||
Db 523 ELDETLAPYIPMDGEDFQL 542
RESULT 36
Q9XTA4 PRELIMINARY; PRT; 870 AA.
AC Q9XTA4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endothelial PAS domain protein 1/hypoxia-inducible factor-2
DE alpha.
DE alpha.
GN Name=EPAS1/HIF2 alpha;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCB TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Arterial;
RX MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA Hara S., Kobayashi C., Imura N.;
RT "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-
1alpha and -2alpha of bovine arterial endothelial cells.";
RL Biochim. Biophys. Acta 1445:237-243 (1999).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC EMBL; AB018399; BAA78676.1; -;
CC HSSP; Q99814; 1P97.
CC GO; GO:0005634; C:nucleus; IEA.
CC GO; GO:0004871; F:signal transducer activity; IEA.
CC GO; GO:0003700; F:transcription factor activity; IEA.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC GO; GO:0007165; P:signal transduction; IEA.
CC InterPro; IPR001092; HLH_basic.

DR InterPro; IPR001067; Nuc translocat.

DR InterPro; IPR001610; PAC.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAC; 2.

DR PRINTS; PR00785; NCTRNLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAC; 2.

DR PROSITE; PS00888; HLH; 1.

DR PROSITE; PS0112; PAC; 2.

SQ SEQUENCE 870 AA; 96168 MW; FEC602BE6012D7712 CRC64;

Query Match

Best Local Similarity 74.2%; Score 70.5; DB 2; Length 870;

Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAXYIPMD-DDFOL 19

:|||||:|||||:|||||

Db 522 ELDLETLAPYIPMDGEDFOL 541

RESULT 37

Q9PTB3

ID Q9PTB3 PRELIMINARY; PRT; 870 AA.

AC Q9PTB3; (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DE Hypoxia-inducible factor 2 alpha.

OS Coturnix coturnix (Common quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Coturnix.

OX NCBI_TaxID=9091;

RN SEQUENCE FROM N.A.

RP MEDLINE=99425185; PubMed=10495286; DOI=10.1016/S0925-4773(99)00144-6;

RX Elvert G., Lanz S., Kappel A., Flamme I.,

RA "mRNA cloning and expression studies of the quail homolog of HIF-2

RT alpha.";

RL Mech. Dev. 87:193-197(1999).

CC -I- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AF212989; AAF21052.1; --

DR HSSP; Q99814; 1P97

DR GO; GO:0005633; C:nucleus; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR001092; HLH basic.

DR InterPro; IPR001067; Nuc translocat.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAC.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF00785; PAC; 1.

DR Pfam; PF00989; PAC; 2.

DR PRINTS; PR00785; NCTRNLOCATR.

DR SMART; SM00353; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAC; 2.

DR PROSITE; PS00888; HLH; 1.

DR PROSITE; PS0112; PAC; 2.

SQ SEQUENCE 870 AA; 97803 MW; 086AC8CF1639D77C CRC64;

Query Match

Best Local Similarity 74.2%; Score 70.5; DB 2; Length 870;

Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DLDLEMLAXYIPMD-DDFOL 19

:|||||:|||||:|||||

Db 522 ELDLETLAPYIPMDGEDFOL 541

RESULT 38

PAS1_MOUSE

ID PAS1_MOUSE STANDARD; PRT; 874 AA.

AC P97481; O08787; O5046;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2

DE alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (MHLF)

DE (HIF-related factor) (HRF).

GN Name=Epas1; Synonyms=Hif2a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC MEDLINE=97152468; PubMed=9000051;

RA Tian H., McKnight S.L., Russell D.W.;

RT "Endothelial PAS domain protein 1 (EPAS1), a transcription factor

RT selectively expressed in endothelial cells.";

RL Genes Dev. 11:72-82(1997).

[2]

RN SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6; TISSUE=Hypothalamus, and Skeletal muscle;

RX MEDLINE=97272213; PubMed=9113979; DOI=10.1073/pnas.94.9.4273;

RA Ema M., Taya S., Yokotani N., Sogawa K., Matsuda Y.,

RA Fujii-Kuriyama Y.;

RT "A novel bHLH-PAS factor with close sequence similarity to hypoxia-

RT inducible factor alpha regulates the VEGF expression and is

RT potentially involved in lung and vascular development.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).

[3]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain capillary;

RC MEDLINE=97321546; PubMed=9178256; DOI=10.1016/S0925-4773(97)00674-6;

RA Flamme I., Froehlich T., von Reutern M., Kappel A., Damert A.,

RA Risau W.;

RT "HRF, a putative basic helix-loop-helix-PAS-domain transcription

RT factor is closely related to hypoxia-inducible factor-1 alpha and

RT developmentally expressed in blood vessels.";

RL Mech. Dev. 63:51-60(1997).

[4]

RN SEQUENCE OF 846-864, AND MUTAGENESIS OF PRO-530 AND ASN-851.

RC MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;

RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,

RA Bruick R.K.;

RT "FH-1 is an asparaginyl hydroxylase enzyme that regulates the

RT transcriptional activity of hypoxia-inducible factor.";

RL Genes Dev. 16:1466-1471(2002).

[5]

RN INTERACTION WITH CREBBP, PHOSPHORYLATION SITE THR-844, AND MUTAGENESIS

OF THR-844.

RC MEDLINE=22075202; PubMed=11983697; DOI=10.1074/jbc.M201307200;

RA Gradin K., Takasaki C., Fujii-Kuriyama Y., Sogawa K.;

RT "The transcriptional activation function of the HIF-like factor

RT requires phosphorylation at a conserved threonine.";

RL J. Biol. Chem. 277:23508-23514(2002).

[6]

RN HYDROXYLATION OF ASN-851.

RC MEDLINE=21682001; PubMed=11823643; DOI=10.1126/science.1068592;

RA Lando D., Peet D.J., Whelan D.A., Gorman J.J., Whitelaw M.L.;

RT "Asparagine hydroxylation of the HIF transcription domain a hypoxic

RT switch.";

RL Science 295:858-861(2002).

-I- FUNCTION: Transcription factor involved in the induction of oxygen

regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within

the hypoxia response element (HRE) of target gene promoters.

Regulates the vascular endothelial growth factor (VEGF) expression

and seems to be implicated in the development of blood vessels and

the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier. Potent activator of the Tie-2 tyrosine kinase expression. Activation requires recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).

-!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP.

-!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels in lung, followed by heart, kidney, brain and liver. Predominantly expressed in endothelial cells. Also found in smooth muscle cells of the uterus, neurons, and brown adipose tissue. High expression in embryonic choroid plexus and kidney glomeruli.

-!- DEVELOPMENTAL STAGE: In day 11 embryo, expression is almost exclusively seen in endothelial cells of the intersegmental blood vessels separating the somites, the atrial and ventricular chambers of the heart, and the dorsal aorta. High expression also occurs in extra-embryonic membranes. In the developing brain of day 13 embryo, endothelial cells of the highly vascularized choroid plexus contain high levels of EPAS1.

-!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530 by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).

-!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus probably abrogating interaction with CREBBP and EP300 and preventing transcriptional activation.

-!- PTM: Phosphorylated on multiple sites in the CTAD.

-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; U81983; AAB41496.1; -
 EMBL; D89787; BAA20130.1; -
 EMBL; AF045160; AAC12871.1; -
 HSP; O16665; 1H2K.
 TRANSFAC; T02719; -
 MGD; MGI:109169; Epas1.
 InterPro; IPR001092; HLH basic.
 InterPro; IPR001067; Nuc translocat.
 InterPro; IPR001610; PAC.
 InterPro; IPR000014; PAS.
 Pfam; PF00010; HLH; 1.
 Pfam; PF00785; PAC; 1.
 Pfam; PF00989; PAS; 1.
 PRINTS; PR00785; NCTRNLOCATR.
 SMART; SM00353; HLH; 1.
 SMART; SM00086; PAC; 1.
 SMART; SM00091; PAS; 2.
 TIGRFAMs; TIGR00229; sensory_box; 2.
 PROSITE; PS50888; HLH; FALSE_NEG.
 PROSITE; PS50112; PAS; 2.
 KW Activator; Angiogenesis; Developmental protein;
 KW Direct protein sequencing; DNA-binding; Hydroxylation;
 KW Nuclear protein; Phosphorylation; Repeat; Transcription regulation.
 FT DNA_BIND 15 27 Basic motif.
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 NTAD.
 FT DOMAIN 834 874 CTAD.

FT DOMAIN 471 479 Poly-Ser.
 FT MOD_RES 405 Hydroxyproline (By similarity).
 FT MOD_RES 530 Hydroxyproline (By similarity).
 FT MOD_RES 844 844 Phosphothreonine.
 FT MOD_RES 851 851 3-hydroxyasparagine.
 FT MUTAGEN 530 P->A: Confers transcriptional activity at normoxia; when associated with A-851.
 FT MUTAGEN 844 T->A: Decreases interaction with CREBBP.
 FT MUTAGEN 851 N->A: Confers transcriptional activity at normoxia; when associated with A-530.
 FT CONFLICT 25 C->S (in Ref. 2).
 FT CONFLICT 191 K->KS (in Ref. 1).
 FT CONFLICT 439 VS->AA (in Ref. 3).
 FT CONFLICT 463 D->G (in Ref. 3).
 FT CONFLICT 654 G->V (in Ref. 2).
 FT CONFLICT 663 A->P (in Ref. 2).
 FT CONFLICT 669 S->W (in Ref. 1).
 FT CONFLICT 673 P->L (in Ref. 1).
 FT CONFLICT 678 P->L (in Ref. 1).
 FT CONFLICT 725 D->E (in Ref. 3).
 FT CONFLICT 731 P->L (in Ref. 3).
 FT CONFLICT 762 A->G (in Ref. 3).
 FT CONFLICT 786 P->L (in Ref. 3).
 FT CONFLICT 791 P->F (in Ref. 3).
 FT CONFLICT 794 S->N (in Ref. 3).
 SQ SEQUENCE 874 AA; 96712 MW; A6PFA490AE43640C CRC64;
 Query Match 74.2%; Score 70.5; DB 1; Length 874;
 Best Local Similarity 75.0%; Pred. No. 0.027; Mismatches 1; Indels 1; Gaps 1;
 Matches 15; Conservative 3;
 QY 1 DLDLEMLAXYIPMD-DDFQL 19
 :|||||:|||||:|||||
 DB 522 ELDLETLAPYIPMDGEDFQL 541
 RESULT 39
 ID_PASI_RAT STANDARD; PRT; 874 AA.
 AC Q9JHS1;
 DT 10-OCT-2003 (Rel. 42, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha).
 GN Name=Epas1; Synonyms=Hif2a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021.3540531;
 RA Kietzmann T., Cornesse Y., Brechtel K., Modaresi S., Jungermann K.;
 RT "Perivenous expression of the mRNA of the three hypoxia-inducible factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
 RL Biochem. J. 354:531-537(2001).
 CC -!- FUNCTION: Transcription factor involved in the induction of oxygen regulated genes. Binds to core DNA sequence 5'-[AG]CTG-3' within the hypoxia response element (HRE) of target gene promoters. Regulates the vascular endothelial growth factor (VEGF) expression and seems to be implicated in the development of blood vessels and the tubular system of lung. May also play a role in the formation of the endothelium that gives rise to the blood brain barrier. Potent activator of the Tie-2 tyrosine kinase expression. Activation seems to require recruitment of transcriptional coactivators such as CREBBP and probably EP300. Interaction with redox regulatory protein APEX seems to activate CTAD (By similarity).
 CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Heterodimerizes with ARNT (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530
 CC by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
 CC prolines promote interaction with VHL, initiating rapid
 CC ubiquitination and subsequent proteasomal degradation. Under
 CC hypoxia, proline hydroxylation is impaired and ubiquitination is
 CC attenuated, resulting in stabilization (By similarity).
 CC -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus
 CC probably abrogating interaction with CREBBP and EP300 and
 CC preventing transcriptional activation (By similarity).
 CC -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ277828; CAB96612.1; ..
 CC HSSP; Q16665; IH2K.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001067; Nuc translocat.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 2.
 CC PRINTS; PR00785; NCTRNSLOCATR.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC TIGRfam; TIGR00229; sensory_box; 2.
 CC PROSITE; PS50888; HLH; FALSE_NEG.
 CC PROSITE; PS50112; PAS; 2.
 CC Activator; Angiogenesis; Developmental protein; DNA-binding;
 KW Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
 KW Transcription regulation.
 FT DNA_BIND 15 27 Basic motif.
 FT DOMAIN 28 68 Helix-loop-helix motif.
 FT DOMAIN 84 154 PAS 1.
 FT DOMAIN 230 300 PAS 2.
 FT DOMAIN 304 347 PAC.
 FT DOMAIN 495 541 NTAD.
 FT DOMAIN 834 874 CTAD.
 FT DOMAIN 474 479 Poly-Ser.
 FT MOD_RES 405 405 Hydroxyproline (By similarity).
 FT MOD_RES 530 530 Hydroxyproline (By similarity).
 FT MOD_RES 844 844 Phosphothreonine (By similarity).
 FT MOD_RES 851 851 3-hydroxyasparagine (By similarity).
 SQ SEQUENCE 874 AA; 96718 MW; A1F08EB24369796 CRC64;
 Query Match 74.2%; Score 70.5; DB 1; Length 874;
 Best Local Similarity 75.0%; Pred. No. 0.027;
 Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 DLDLEMLAXIIPMD-DDFQL 19
 Db 522 ELDELTAPYIPMDGEDFQL 541
 RESULT 40
 Q6PEU2 PRELIMINARY; PRT; 874 AA.
 AC Q6PEU2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Endothelial PAS domain protein 1.
 GN Name=Epas1;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McWeney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC EMBL; BC057870; AAH57870.1; ..
 CC GO; GO:0005634; C:nucleus; IEA.
 CC GO; GO:0004871; F:signal transducer activity; IEA.
 CC GO; GO:0003700; P:transcription factor activity; IEA.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 CC GO; GO:0007165; P:signal transduction; IEA.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR001067; Nuc translocat.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000014; PAS.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF00785; PAC; 1.
 CC Pfam; PF00989; PAS; 1.
 CC PRINTS; PR00785; NCTRNSLOCATR.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00086; PAC; 1.
 CC SMART; SM00091; PAS; 2.
 CC PROSITE; PS50112; PAS; 2.
 SQ SEQUENCE 874 AA; 96636 MW; 2E6D7603A678EACE CRC64;
 Query Match 74.2%; Score 70.5; DB 2; Length 874;
 Best Local Similarity 75.0%; Pred. No. 0.027;
 Matches 15; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 DLDLEMLAXIIPMD-DDFQL 19
 Db 522 ELDELTAPYIPMDGEDFQL 541
 RESULT 41
 Q8QG15 PRELIMINARY; PRT; 235 AA.
 ID Q8QG15
 AC Q8QG15;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypoxia-inducible factor alpha-like protein (Fragment).
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
RA Powell W.H., Hahn M.E.;
RT "Identification and functional characterization of hypoxia-inducible
RT factor 2alpha from the estuarine teleost, Fundulus heteroclitus:
RT interaction of HIF-2alpha with two ARNT2 splice variants.";
RL J. Exp. Zool. 294:17-29(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Oleksiak M.F., Kellell K.J., Crawford D.L., Hahn M.E., Powell W.H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF433668; AAM12473.1; -;
DR HSSP; Q99814; 1P97.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001610; PAC.
DR SMART; SM00086; PAC; 1.
FT NON_TER 1
FT NON_TER 235
SQ SEQUENCE 235 AA; 25400 MW; AE7A7C5D15827351 CRC64;

Query Match 62.1%; Score 59; DB 2; Length 235;
Best Local Similarity 73.3%; Pred. No. 0.48;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLEMLAXYIPMDDDF 17
DB 221 ELEMAYIPISMDDDP 235

RESULT 42
Q9AGM7
ID Q9AGM7 PRELIMINARY; PRT; 494 AA.
AC Q9AGM7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type II protein secretion ATPase LepE.
GN Name=lepE;
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=130b;
RX MEDLINE=21153567; PubMed=11254562;
RX DOI=10.1128/IAI.69.4.2092-2098.2001;
RA Rossier O., Cianciotto N.P.;
RT "Type II protein secretion is a subset of the PilD-dependent processes
RT that facilitate intracellular infection by Legionella pneumophila.";
RL Infect. Immun. 69:2092-2098(2001).
DR EMBL; AF330136; AAK35046.1; -;
DR HSSP; P37093; 1P9R.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR Pfam; PF00437; GSP11_E; 1.
DR InterPro; IPR001482; GSP11_E.
DR ProDom; PD000739; GSP11_E; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00662; T2SP_E; 1.
KW ATP-binding.
SQ SEQUENCE 494 AA; 55138 MW; E81B27C741036B0C CRC64;

Query Match 51.6%; Score 49; DB 2; Length 494;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLDLEMLAXYIPMDDD 16
DB 88 DMDLSMLASQLFVSED 103

RESULT 43
Q8JZM8
ID Q8JZM8 PRELIMINARY; PRT; 339 AA.
AC Q8JZM8
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase SNF.
GN Name=snf;
OS Colletotrichum gloeosporioides f. sp. malvae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=96478;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22286319; PubMed=12399031;
RA Goodwin P.H., Chen G.Y.-J.;
RT "High expression of a sucrose non-fermenting (SNF1)-related protein
RT kinase from Colletotrichum gloeosporioides f. sp. malvae is associated
RT with penetration of Malva pusilla.";
RL FEMS Microbiol. Lett. 215:169-174(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22443387; PubMed=12556131;
RA Goodwin P.H., Chen G.Y.-J.;
RT "Expression of a glycogen synthase protein kinase homolog from
RT Colletotrichum gloeosporioides f. sp. malvae during infection of Malva
RT pusilla.";
RL Can. J. Microbiol. 48:1035-1039(2002).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF421215; AAN32717.1; -;
DR HSSP; P31751; 1MRY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR PRINTS; PR001245; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 339 AA; 37330 MW; 58F5BB0D3E2AB476 CRC64;

Query Match 50.5%; Score 48; DB 2; Length 339;
Best Local Similarity 72.7%; Pred. No. 40;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDD 16
DB 274 MLAGYLPEDDD 284

RESULT 44
Q72993

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ID Q72993 PRELIMINARY; PRT; 492 AA.
AC Q72993;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE SPAC110.01 protein (spac110.05 protein) (Fragment).
GN Name=SPAC110.01; Synonyms=SPAC140.05;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby I., Howarth S., Huckle E.J., Hunt S., Jørgensen K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quayl M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.-J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard J., Talla V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL441624; CAD99127.1; -.
DR HSSP; O14757; 1I48.
DR GeneDB_Sponge; SPAC110.01; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001109; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN KINASE ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 492 AA; 55160 MW; 7352D9C14868982F CRC64;

Query Match 50.5%; Score 48; DB 2; Length 492;
Best Local Similarity 72.7%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 MLAXYIPWDDD 16
DB 175 MLAGYLPFDDDD 185

RESULT 45
KIN4_YEAST
ID KIN4_YEAST STANDARD; PRT; 800 AA.
AC Q01919;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase KIN4 (EC 2.7.1.37).
GN Name=KIN4; Synonyms=KIN3, KIN31; OrderedLocusNames=YOR233W;
GN ORFNames=O5220;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97127829; PubMed=8972580;
RX DOI=10.1002/(SICI)1097-0061(199612)12:15<1575::AID-YEA45>3.3.CO;2-5;
RA Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.;
RT "Sequence and analysis of a 26.9 kb fragment from chromosome XV of the
RT yeast Saccharomyces cerevisiae."
RL Yeast 12:1575-1586(1996).
CC -1- FUNCTION: This protein is probably a serine/threonine protein
CC Kinase.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X67916; CAA48115.1; -.
DR EMBL; Z75141; CAA99453.1; -.
DR PIR; S29344; S29344.
DR HSSP; Q63450; 1A06.
DR GerMOnline; 143821; -.
DR SGD; S000005759; KIN4.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 46 313
FT NP_BIND 52 60
FT BINDING 80 80
FT ACT_SITE 175 175
FT ACT_SITE 175 175
SQ SEQUENCE 800 AA; 90087 MW; 655BBB5EBD8ACF65 CRC64;

Query Match 50.5%; Score 48; DB 1; Length 800;
Best Local Similarity 61.5%; Pred. No. 97;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 MLAXYIPWDDDDQ 18
DB 245 MLAGYLPWDDDDHE 257

RESULT 46
```

Q5BTQ3
ID O6BTQ3 PRELIMINARY; PRT; 979 AA.
AC Q6BTQ3
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Similar to CA2348|IPF12811 Candida albicans.
GN ORFNames=DEHAOC179969;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OC NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genocleures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anchoard V., Sabour A., Barbé V.,
RA Barnay S., Blanchin L., Beckerich J.M., Beyne E., Bleykaesten C.,
RA Boirame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; CR382135; CAG86498.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR008271; Ser thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 979 AA; 108438 MW; 277DA42CF95137FD CRC64;

Query Match 50.5%; Score 48; DB 2; Length 979;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDDD 16
|||:|:|
DB 234 MLAGLPPFDDDD 244
|||:|:|

RESULT 47
Q7SFD3 PRELIMINARY; PRT; 1168 AA.
AC Q7SFD3
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein (Related to ser/thr protein kinase KIN4).
GN Name=NCU00914.1; Synonyms=B13C5.030;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseis M., Maucell E., Bielke C., Rudd S., Frisman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Navig D.O., Alex L.A., Mannhaupt G., Ebbels D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC German Neurospora genome project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100021; EAA35504.1; -.
DR EMBL; BX842682; CAE81987.1; -.
DR HSPF; O14757; IIA8.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Ser thr kinase.
DR InterPro; IPR008271; Ser thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1168 AA; 127404 MW; C4828C040483820C CRC64;

Query Match 50.5%; Score 48; DB 2; Length 1168;
Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 MLAXYIPMDDDD 16
|||:|:|
DB 533 MLAGLPPFDDDD 543
|||:|:|

RESULT 48
SINA DROME STANDARD; PRT; 1507 AA.
ID SINA DROME
AC Q24167; Q9VAA5;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Similar protein.
 DE Names=sima; ORFNames=CG7951;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96269413; PubMed=8692312; DOI=10.1016/0378-1119(96)00060-1;
 RY Nambu J.R., Chen W., Hu S., Crews S.T.;
 RT "The Drosophila melanogaster bHLH-PAS gene encodes a protein
 RT related to human hypoxia-inducible factor 1 alpha and Drosophila
 RT single-minded";
 RL Gene 172:249-254 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Acavani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 RN [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Snu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.22(2002).
 CC -!- FUNCTION: Possible DNA-binding transcriptional activator.
 CC -!- SUBUNIT: Efficient DNA-binding requires dimerization with another

bHLH protein.
 -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 -!- TISSUE SPECIFICITY: Ubiquitously expressed in the embryo.
 -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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 or send an email to license@isb-sib.ch).

 EMBL; U43090; AAC47303.1; -.
 EMBL; AE003772; AAF57008.2; -.
 DR PIR; JC4851; JC4851.
 DR FlyBase; FBgn0015542; sima.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.
 DR Pfam; PF00785; PAS; 1.
 DR Pfam; PF00989; PAS; 1.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS00888; HLH; FALSE_NEG.
 DR PROSITE; PS01112; PAS; 2.
 KW Activator; Coiled coil; DNA-binding; Nuclear protein; Repeat;
 KW Transcription regulation.
 FT DNA BIND 72 85 Basic motif.
 FT DOMAIN 86 126 Helix-loop-helix motif (By similarity).
 FT DOMAIN 167 240 PAS 1.
 FT DOMAIN 307 377 PAS 2.
 FT DOMAIN 381 422 PAC.
 FT DOMAIN 577 587 Pro-rich.
 FT DOMAIN 880 908 Coiled coil (Potential).
 FT DOMAIN 982 1054 Coiled coil (Potential).
 FT DOMAIN 1110 1162 Coiled coil (Potential).
 FT DOMAIN 26 39 Poly-Ser.
 FT DOMAIN 718 725 Poly-Ser.
 FT DOMAIN 759 763 Poly-Gln.
 FT DOMAIN 767 776 Poly-Gln.
 FT DOMAIN 907 918 Poly-Gln.
 FT DOMAIN 945 948 Poly-Gln.
 FT DOMAIN 990 998 Poly-Gln.
 FT DOMAIN 1020 1038 Poly-Gln.
 FT DOMAIN 1113 1126 Poly-Gln.
 FT DOMAIN 1146 1162 Poly-Gln.
 FT DOMAIN 1205 1208 Poly-Gln.
 FT DOMAIN 1277 1284 Poly-Gln.
 FT DOMAIN 1298 1301 Poly-Asp.
 FT DOMAIN 38 38 S -> A (in Ref. 1).
 FT DOMAIN 345 345 S -> L (in Ref. 1).
 FT DOMAIN 492 492 A -> V (in Ref. 1).
 FT DOMAIN 588 588 T -> I (in Ref. 1).
 FT DOMAIN 709 709 T -> K (in Ref. 1).
 FT DOMAIN 776 776 Q -> QQQQ (in Ref. 1).
 FT DOMAIN 895 895 Q -> QQ (in Ref. 1).
 FT DOMAIN 902 902 G -> S (in Ref. 1).
 FT DOMAIN 982 982 A -> T (in Ref. 1).
 FT DOMAIN 1125 1126 Missing (in Ref. 1).
 FT DOMAIN 1154 1157 Missing (in Ref. 1).
 FT DOMAIN 1444 1444 F -> L (in Ref. 1).
 FT DOMAIN 1447 1447 G -> C (in Ref. 1).
 FT DOMAIN 1451 1451 S -> N (in Ref. 1).
 FT DOMAIN 1494 1494 D -> G (in Ref. 1).
 SQ SEQUENCE 1507 AA; 165824 MW; 4102939C8FBFB0C6 CRC64;
 Query Match 50.5%; Score 48; DB 1; Length 1507;
 Best Local Similarity 64.3%; Pred. No. 1.9e+02;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;


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Qy 6 MLAXYIPWDDDFQ 19
| : : : : :
Db 847 MRAPYIPIDDDMPL 860

RESULT 49
Q6FPH1
ID Q6FPH1 PRELIMINARY; PRT; 661 AA.
AC Q6FPH1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome J complete sequence.
GN ORFNames=CAGLQJ03872g;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
EG Geoleiursea;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Catillico L., Confaniolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekaiia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; CR380956; CAG60822.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; STK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 661 AA; 74754 MW; CCA17EAC686472D3 CRC64;

Query Match 49.5%; Score 47; DB 2; Length 661;
Best Local Similarity 72.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 MLAXYIPWDDD 16
| : : : :
Db 248 MLAGYLPWDDD 258

RESULT 50
Q7T838
ID Q7T838 PRELIMINARY; PRT; 688 AA.
AC Q7T838

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphotransferase pUL97 (Fragment).
GN Name=UL97;
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RA Alain S., Courdault L., Ducancelle A., Hantz S., Cogne N.,
RA Champier G., Duverlie G., Honderlick P., Thouvenot D., Najjoulah F.,
RA Fillet A.M., Gouarin S.P., Sanson Le Pors M.E., Denis F.O.,
RA Mazon M.C.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF520960; AAP87552.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR010615; UL97.
DR Pfam; PF06734; UL97; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW Transferase.
FT NON_TER 688
SQ SEQUENCE 688 AA; 76086 MW; 54AE51AFF84493B3 CRC64;

Query Match 49.5%; Score 47; DB 2; Length 689;
Best Local Similarity 41.2%; Pred. No. 1.2e+02;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLDLEMLAXYIPMDDDF 17
| : : : :
Db 304 ELSISYLLVYVPKEDDF 320

Search completed: February 8, 2005, 20:09:54
Job time : 97.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 8.2807 Seconds
(without alignments)
72.119 Million cell updates/sec

Title: US-10-032-361-4
Perfect score: 41
Sequence: 1 MLAPTIPM 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : Issued Patents AA*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	82.9	19	4	US-09-959-873B-8
2	34	82.9	34	4	US-09-959-873B-9
3	34	82.9	54	4	US-09-438-833-13
4	34	82.9	116	4	US-09-438-833-8
5	34	82.9	266	4	US-09-252-991A-23473
6	34	82.9	288	4	US-09-438-833-9
7	34	82.9	301	4	US-09-438-833-10
8	34	82.9	311	4	US-09-438-833-7
9	34	82.9	532	4	US-09-949-016-7389
10	34	82.9	613	4	US-09-438-833-6
11	34	82.9	652	4	US-09-438-833-5
12	34	82.9	756	4	US-09-438-833-11
13	34	82.9	805	2	US-08-480-473B-4
14	34	82.9	805	3	US-08-915-213-4
15	34	82.9	805	3	US-09-235-217-4
16	34	82.9	805	5	PCT-US96-10251-4
17	34	82.9	810	1	US-08-785-241-7
18	34	82.9	813	4	US-09-438-833-12
19	34	82.9	826	1	US-08-785-241-6
20	34	82.9	826	2	US-08-480-473B-2
21	34	82.9	826	3	US-08-915-213-2
22	34	82.9	826	3	US-09-148-547-2
23	34	82.9	826	3	US-09-235-217-2
24	34	82.9	826	3	US-09-380-662-23
25	34	82.9	826	4	US-09-438-833-1
26	34	82.9	826	4	US-09-702-705-330
27	34	82.9	826	4	US-09-736-457-330

28	34	82.9	826	4	US-09-383-581-2	Sequence 2, Appli
29	34	82.9	826	4	US-09-614-124B-330	Sequence 330, App
30	34	82.9	826	4	US-09-671-325-330	Sequence 330, App
31	34	82.9	826	4	US-09-589-184-330	Sequence 330, App
32	34	82.9	826	4	US-09-658-824-330	Sequence 330, App
33	34	82.9	826	4	US-09-959-873B-18	Sequence 18, Appli
34	34	82.9	826	4	US-09-949-016-6089	Sequence 6089, Ap
35	34	82.9	826	4	US-09-967-388-4	Sequence 4, Appli
36	34	82.9	826	5	PCT-US96-10251-2	Sequence 2, Appli
37	34	82.9	827	4	US-09-919-039-149	Sequence 149, App
38	33	80.5	463	4	US-09-902-540-15324	Sequence 15324, A
39	33	80.5	785	4	US-09-248-796A-24492	Sequence 24492, A
40	32	78.0	499	4	US-03-270-767-46796	Sequence 46796, A
41	32	78.0	1420	4	US-09-902-540-11946	Sequence 11946, A
42	31	75.6	73	3	US-09-041-889-12	Sequence 12, Appli
43	31	75.6	73	3	US-08-837-058-12	Sequence 12, Appli
44	31	75.6	73	4	US-09-417-264-12	Sequence 12, Appli
45	31	75.6	86	4	US-09-252-991A-20923	Sequence 20923, A
46	31	75.6	117	4	US-09-640-211A-689	Sequence 689, App
47	31	75.6	151	4	US-09-732-210-202	Sequence 202, App
48	31	75.6	220	3	US-09-041-889-2	Sequence 2, Appli
49	31	75.6	220	3	US-08-837-058-2	Sequence 2, Appli
50	31	75.6	220	4	US-09-417-264-2	Sequence 2, Appli
51	31	75.6	221	4	US-09-949-016-8205	Sequence 8205, Ap
52	30	73.2	91	4	US-09-513-999C-7147	Sequence 7147, Ap
53	30	73.2	174	4	US-09-252-991A-26812	Sequence 26812, A
54	30	73.2	466	2	US-08-726-136-28	Sequence 28, Appli
55	30	73.2	466	3	US-09-103-434-28	Sequence 28, Appli
56	30	73.2	466	3	US-09-687-594-28	Sequence 28, Appli
57	30	73.2	553	4	US-09-252-991A-32621	Sequence 32621, A
58	30	73.2	610	4	US-09-455-777-2	Sequence 2, Appli
59	30	73.2	634	4	US-09-614-912-88	Sequence 88, Appli
60	30	73.2	634	4	US-09-614-912-100	Sequence 100, App
61	30	73.2	1200	4	US-09-644-827B-8	Sequence 8, Appli
62	30	73.2	1428	4	US-09-644-827B-7	Sequence 7, Appli
63	29	70.7	8	4	US-09-959-873B-1	Sequence 1, Appli
64	29	70.7	67	4	US-09-252-991A-26471	Sequence 26471, A
65	29	70.7	121	4	US-09-902-540-10258	Sequence 10258, A

ALIGNMENTS

RESULT 1
US-09-959-873B-8
; Sequence 8, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-09-959-873B-8
Query Match 82.9%; Score 34; DB 4; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.8;

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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
Db 6 MLAPVIMP 13

RESULT 2
US-09-959-873B-9
; Sequence 9, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-959-873B-9

Query Match 82.9%; Score 34; DB 4; Length 34;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
Db 13 MLAPVIMP 20

RESULT 3
US-09-438-833-13
; Sequence 13, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
US-09-438-833-13

Query Match 82.9%; Score 34; DB 4; Length 54;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
Db 31 MLAPVIMP 38
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RESULT 4
US-09-438-833-8
; Sequence 8, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
US-09-438-833-8

Query Match 82.9%; Score 34; DB 4; Length 116;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
Db 36 MLAPVIMP 43

RESULT 5
US-09-252-991A-23473
; Sequence 23473, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23473
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23473

Query Match 82.9%; Score 34; DB 4; Length 266;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
Db 163 MLAPVIMP 170

RESULT 6
US-09-438-833-9
; Sequence 9, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-813 of human HIF-1 alpha
US-09-438-833-9

Query Match 82.9%; Score 34; DB 4; Length 288;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIMP 8
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Db 36 MLAPYIPM 43

RESULT 7
US-09-438-833-10
; Sequence 10, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-826 of human HIF-1 alpha
US-09-438-833-10

Query Match 82.9%; Score 34; DB 4; Length 301;
Best Local Similarity 87.5%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIMP 8
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Db 36 MLAPYIPM 43

RESULT 8
US-09-438-833-7
; Sequence 7, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 331-641 of human HIF-1 alpha
US-09-438-833-7

Query Match 82.9%; Score 34; DB 4; Length 311;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIMP 8
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Db 231 MLAPYIPM 238

RESULT 9
US-09-949-016-7389
; Sequence 7389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7389
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7389

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Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIMP 8
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Db 267 MLAPYIPM 274

RESULT 10
US-09-438-833-6
; Sequence 6, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-438-833-6

Query Match 82.9%; Score 34; DB 4; Length 613;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIMP 8
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Db 348 MLAPYIPM 355

RESULT 11
US-09-438-833-5
; Sequence 5, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn

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; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-652 of human HIF-1 alpha
US-09-438-833-5

Query Match      82.9%; Score 34; DB 4; Length 652;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPYIPM 8
Db      561 MLAPYIPM 568

RESULT 12
US-09-438-833-11
; Sequence 11, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 71-826 of human HIF-1 alpha
US-09-438-833-11

Query Match      82.9%; Score 34; DB 4; Length 756;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPYIPM 8
Db      491 MLAPYIPM 498

RESULT 13
US-08-480-473B-4
; Sequence 4, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-480-473B-4

Query Match      82.9%; Score 34; DB 2; Length 805;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPYIPM 8
Db      540 MLAPYIPM 547

RESULT 14
US-08-915-213-4
; Sequence 4, Application US/08915213
; Patent No. 6020462
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/915,213
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-915-213-4

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/480,473B
; APPLICATION NUMBER: 07265/053001
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-915-213-4
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Query Match 82.9%; Score 34; DB 3; Length 805;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
Db 540 MLAPVPM 547

RESULT 15
US-09-235-217-4
; Sequence 4, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-217-4

Query Match 82.9%; Score 34; DB 3; Length 805;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
Db 540 MLAPVPM 547

RESULT 16
PCT-US96-10251-4
; Sequence 4, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA

; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10251-4

Query Match 82.9%; Score 34; DB 5; Length 805;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
Db 540 MLAPVPM 547

RESULT 17
US-08-785-241-7
; Sequence 7, Application US/08785241
; Patent No. 5695963
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.
; APPLICANT: Tian, Hui
; TITLE OF INVENTION: Endothelial PAS Domain Protein
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,241
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UTSD:1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 amino acids
; TYPE: amino acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-241-7

Query Match      82.9%; Score 34; DB 1; Length 810;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLAPTIPM 8
Db      548 MLAPYIPM 555

RESULT 18
US-09-438-833-12
; Sequence 12, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 813
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-813 Of human HIF-1 alpha
US-09-438-833-12

Query Match      82.9%; Score 34; DB 4; Length 813;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLAPTIPM 8
Db      561 MLAPYIPM 568

RESULT 19
US-08-785-241-6
; Sequence 6, Application US/08785241
; Patent No. 5695963
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L.
; APPLICANT: Russell, David W.
; APPLICANT: Tian, Hui
; TITLE OF INVENTION: Endothelial PAS Domain Protein
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,241
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UTSD:1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-241-6

Query Match      82.9%; Score 34; DB 1; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLAPTIPM 8
Db      561 MLAPYIPM 568

RESULT 20
US-08-480-473B-2
; Sequence 2, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-473B-2

Query Match      82.9%; Score 34; DB 2; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLAPTIPM 8
Db      561 MLAPYIPM 568

RESULT 21
US-08-915-213-2
; Sequence 2, Application US/08915213
```


Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-213-2

Query Match 82.9%; Score 34; DB 3; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPITPM 8
Db 561 MLAPYIPM 568

RESULT 22
US-09-148-547-2
Sequence 2, Application US/09148547
Patent No. 6124131
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
FILE REFERENCE: 07265/151001
CURRENT APPLICATION NUMBER: US/09/148,547
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 826
TYPE: PRT
ORGANISM: Homo sapiens
US-09-148-547-2

Query Match 82.9%; Score 34; DB 3; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPITPM 8
Db 561 MLAPYIPM 568

RESULT 23
US-09-235-217-2
Sequence 2, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,217
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-235-217-2

Query Match 82.9%; Score 34; DB 3; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPITPM 8
Db 561 MLAPYIPM 568

RESULT 24
US-09-380-662-23
Sequence 23, Application US/09380662
Patent No. 6376199
GENERAL INFORMATION:
APPLICANT: Caniggia, Isabella
APPLICANT: Post, Martin
APPLICANT: Lye, Stephen
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
FILE REFERENCE: 11757.38USWO
CURRENT APPLICATION NUMBER: US/09/380,662
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: US 60/039,919
PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 826

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-23

Query Match 82.9%; Score 34; DB 3; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
|||||
Db 561 MLAPYIPM 568

RESULT 25
US-09-438-833-1
; Sequence 1, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 92
; PAGES: 5510-5514
; DATABASE ACCESSION NUMBER: GenBank U22431
; DATABASE ENTRY DATE: 1995-06-28
US-09-438-833-1

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
|||||
Db 561 MLAPYIPM 568

RESULT 26
US-09-702-705-330
; Sequence 330, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-330

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
|||||
Db 561 MLAPYIPM 568

RESULT 27
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
|||||
Db 561 MLAPYIPM 568

RESULT 28
US-09-383-581-2
; Sequence 2, Application US/09383581
; Patent No. 6562799
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/09/383,581
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-581-2

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568

```
RESULT 29
US-09-614-124B-330
; Sequence 330, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-330
```

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568

```
RESULT 30
US-09-671-325-330
; Sequence 330, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-330
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Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568

```
RESULT 31
US-09-589-184-330
; Sequence 330, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-330
```

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568

```
RESULT 32
US-09-658-824-330
; Sequence 330, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-330
```

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568

RESULT 33

US-09-959-873B-18
; Sequence 18, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-873B-18

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIM 8
| | | | |
Db 561 MLAPYIPM 568

RESULT 34
US-09-949-016-6089
; Sequence 6089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6089
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6089

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIM 8
| | | | |
Db 561 MLAPYIPM 568

RESULT 35
US-09-967-388-4
; Sequence 4, Application US/09967388
; Patent No. 6838430
; GENERAL INFORMATION:

; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; TITLE OF INVENTION: WOUND HEALING
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match 82.9%; Score 34; DB 4; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIM 8
| | | | |
Db 561 MLAPYIPM 568

RESULT 36
PCT-US96-10251-2
; Sequence 2, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10251-2

Query Match 82.9%; Score 34; DB 5; Length 826;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIM 8
| | | | |
Db 561 MLAPYIPM 568

RESULT 37
US-09-919-039-149
; Sequence 149, Application US/09919039

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; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CD1
US-09-919-039-149

Query Match      82.9%; Score 34; DB 4; Length 827;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      562 MLAPYIPM 569

RESULT 38
US-09-902-540-15324
; Sequence 15324, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15324
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15324

Query Match      80.5%; Score 33; DB 4; Length 463;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LAPTIPM 8
Db      122 LAPTIPM 128

RESULT 39
US-09-248-796A-24492
; Sequence 24492, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
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; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24492
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (12),(240)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-24492

Query Match      80.5%; Score 33; DB 4; Length 785;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      229 MLPTPL 236

RESULT 40
US-09-270-767-46796
; Sequence 46796, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46796
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46796

Query Match      78.0%; Score 32; DB 4; Length 499;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      443 ILIPTIPM 450

RESULT 41
US-09-902-540-11946
; Sequence 11946, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11946
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11946
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Query Match      78.0%; Score 32; DB 4; Length 1420;
Best Local Similarity 71.4%; Pred. No. 9,7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LAPTIPM 8
DB      217 LAPTIVPL 223

RESULT 42
US-09-041-889-12
; Sequence 12, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-041-889-12

Query Match      75.6%; Score 31; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LAPTIP 7
DB      6 LAPTIP 11

RESULT 43
US-08-837-058-12
; Sequence 12, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Targan, Stephan R.
; APPLICANT: Eggens, Mark
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Histone H1

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; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,058
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 2438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-837-058-12

Query Match      75.6%; Score 31; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LAPTIP 7
DB      6 LAPTIP 11

RESULT 44
US-09-417-264-12
; Sequence 12, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,889
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

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REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-417-264-12

Query Match 75.6%; Score 31; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAPTIP 7
DB 6 LAPTIP 11

RESULT 45
US-09-252-991A-20923
Sequence 20923, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20923
LENGTH: 86
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20923

Query Match 75.6%; Score 31; DB 4; Length 86;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAPTIP 7
DB 37 VLAPTVP 43

RESULT 46
US-09-640-211A-689
Sequence 689, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 689
LENGTH: 117
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-640-211A-689

Query Match 75.6%; Score 31; DB 4; Length 117;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIP 8
DB 67 MLOPTLPL 74

RESULT 47
US-09-732-210-202
Sequence 202, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jibong
APPLICANT: Mitanok, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 202
LENGTH: 151
TYPE: PRT
ORGANISM: Lumbricus rubellus
US-09-732-210-202

Query Match 75.6%; Score 31; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAPTIP 7
DB 80 LAPTIP 85

RESULT 48
US-09-041-889-2
Sequence 2, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997

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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:57:42 ; Search time 107.649 Seconds
(without alignments)
24.205 Million cell updates/sec

Title: US-10-032-361-4
Perfect score: 41
Sequence: 1 MLAPTPM 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	87.8	8	14 US-10-101-662A-20	Sequence 20, Appl
2	36	87.8	8	14 US-10-287-670-20	Sequence 20, Appl
3	35	85.4	528	16 US-10-437-963-116010	Sequence 116010,
4	34	82.9	8	14 US-10-101-662A-16	Sequence 16, Appl
5	34	82.9	8	14 US-10-101-816-8	Sequence 8, Appl
6	34	82.9	8	14 US-10-287-670-16	Sequence 16, Appl
7	34	82.9	19	16 US-10-901-583-8	Sequence 8, Appl
8	34	82.9	20	14 US-10-287-670-25	Sequence 25, Appl
9	34	82.9	34	16 US-10-901-583-9	Sequence 9, Appl
10	34	82.9	54	9 US-09-922-958-5	Sequence 5, Appl
11	34	82.9	409	15 US-10-425-833-8	Sequence 8, Appl
12	34	82.9	466	15 US-10-425-833-9	Sequence 9, Appl
13	34	82.9	538	15 US-10-425-833-6	Sequence 6, Appl

14	34	82.9	542	15	US-10-364-049-2606	Sequence 2606, App
15	34	82.9	595	15	US-10-425-833-7	Sequence 7, Appl
16	34	82.9	632	15	US-10-425-833-10	Sequence 10, Appl
17	34	82.9	823	14	US-10-205-342-13	Sequence 13, Appl
18	34	82.9	826	9	US-09-922-958-4	Sequence 4, Appl
19	34	82.9	826	9	US-08-833-750-235	Sequence 235, App
20	34	82.9	826	9	US-09-736-457-330	Sequence 330, App
21	34	82.9	826	9	US-09-902-941-330	Sequence 330, App
22	34	82.9	826	9	US-09-849-626-330	Sequence 330, App
23	34	82.9	826	10	US-09-967-388-4	Sequence 4, Appl
24	34	82.9	826	10	US-09-476-300-330	Sequence 330, App
25	34	82.9	826	13	US-10-028-158-23	Sequence 23, Appl
26	34	82.9	826	13	US-10-101-812-10	Sequence 10, Appl
27	34	82.9	826	14	US-10-101-662A-9	Sequence 9, Appl
28	34	82.9	826	14	US-10-017-754-330	Sequence 330, App
29	34	82.9	826	14	US-10-115-987B-14	Sequence 14, Appl
30	34	82.9	826	14	US-10-287-670-9	Sequence 9, Appl
31	34	82.9	826	14	US-10-113-872-330	Sequence 330, App
32	34	82.9	826	14	US-10-423-419-2	Sequence 2, Appl
33	34	82.9	826	15	US-10-283-017-330	Sequence 330, App
34	34	82.9	826	16	US-10-901-583-18	Sequence 18, Appl
35	34	82.9	827	10	US-09-919-039-149	Sequence 149, App
36	34	82.9	827	14	US-10-247-671-137	Sequence 137, App
37	33	80.5	57	15	US-10-424-599-264106	Sequence 264106, App
38	33	80.5	104	15	US-10-264-237-1843	Sequence 1843, App
39	33	80.5	147	16	US-10-437-963-148789	Sequence 148789, App
40	33	80.5	168	16	US-10-437-963-201061	Sequence 201061, App
41	33	80.5	169	16	US-10-437-963-109991	Sequence 109991, App
42	33	80.5	173	16	US-10-437-963-109635	Sequence 109635, App
43	33	80.5	173	16	US-10-437-963-109941	Sequence 109941, App
44	33	80.5	181	16	US-10-437-963-104575	Sequence 104575, App
45	33	80.5	195	16	US-10-437-963-109898	Sequence 109898, App
46	33	80.5	207	16	US-10-437-963-202314	Sequence 202314, App
47	33	80.5	231	16	US-10-437-963-134864	Sequence 134864, App
48	33	80.5	1557	16	US-10-437-963-137427	Sequence 137427, App
49	33	80.5	2017	16	US-10-437-963-204305	Sequence 204305, App
50	32	78.0	139	16	US-10-437-963-184153	Sequence 184153, App
51	32	78.0	143	16	US-10-437-963-116767	Sequence 116767, App
52	32	78.0	145	14	US-10-156-761-14561	Sequence 14561, A
53	32	78.0	180	16	US-10-437-963-149829	Sequence 149829, App
54	32	78.0	245	16	US-10-437-963-109960	Sequence 109960, App
55	32	78.0	264	16	US-10-437-963-109853	Sequence 109853, App
56	32	78.0	270	15	US-10-425-114-49540	Sequence 49540, A
57	32	78.0	392	15	US-10-424-599-158119	Sequence 158119, App
58	32	78.0	404	16	US-10-437-963-162793	Sequence 162793, App
59	32	78.0	802	16	US-10-437-963-116769	Sequence 116769, App
60	32	78.0	819	16	US-10-437-963-113827	Sequence 113827, App
61	32	78.0	9234	10	US-09-942-025-13	Sequence 13, Appl
62	31	75.6	55	15	US-10-424-599-152902	Sequence 152902, App
63	31	75.6	73	14	US-10-229-567-12	Sequence 12, Appl
64	31	75.6	74	15	US-10-424-599-169556	Sequence 169556, App
65	31	75.6	88	14	US-10-029-386-33979	Sequence 33979, A

ALIGNMENTS

RESULT 1
US-10-101-662A-20
; Sequence 20, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10101.662A
; PRIORITY FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431

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/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/277,440
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/332,493
/ PRIOR FILING DATE: 2001-11-09
/ PRIOR APPLICATION NUMBER: 60/345,131
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/342,598
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/345,132
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/332,334
/ PRIOR FILING DATE: 2001-11-09
/ PRIOR APPLICATION NUMBER: 60/345,200
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 20
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:synthetic
/ OTHER INFORMATION: peptide
US-10-101-662A-20
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Query Match      87.8%; Score 36; DB 14; Length 8;
Best Local Similarity 87.5%; Pred.No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 MLAPTIPM 8
      |||||
Db      1 MLAPAIPM 8
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RESULT 2

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US-10-287-670-20
/ Sequence 20, Application US/10287670
/ Publication No. US20030150005A1
/ GENERAL INFORMATION:
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/ APPLICANT: Kaelin Jr., et al.
/ TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
/ TITLE OF INVENTION: Diagnostic and
/ TITLE OF INVENTION: Therapeutic Methods Thereof
/ FILE REFERENCE: 20363-009CIP1
/ CURRENT APPLICATION NUMBER: US/10/287,670
/ CURRENT FILING DATE: 2003-02-20
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/ PRIOR APPLICATION NUMBER: 10/101,662
/ PRIOR FILING DATE: 2002-03-19
/ PRIOR APPLICATION NUMBER: 10/101,812
/ PRIOR FILING DATE: 2002-03-19
/ PRIOR APPLICATION NUMBER: 10/101,816
/ PRIOR FILING DATE: 2002-03-19
/ PRIOR APPLICATION NUMBER: 60/277,425
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/277,431
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/277,440
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/332,493
/ PRIOR FILING DATE: 2001-11-09
/ PRIOR APPLICATION NUMBER: 60/345,131
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/342,598
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/345,132
/ PRIOR FILING DATE: 2001-12-20
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 25
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/ SOFTWARE: PatentIn Ver. 2.1
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/ SEQ ID NO 20
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/ LENGTH: 8
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/ TYPE: PRT
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/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:synthetic
/ OTHER INFORMATION: peptide
US-10-287-670-20
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```
Query Match      87.8%; Score 36; DB 14; Length 8;
Best Local Similarity 87.5%; Pred.No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 MLAPTIPM 8
      |||||
Db      1 MLAPAIPM 8
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RESULT 3

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US-10-437-963-116010
/ Sequence 116010, Application US/10437963
/ Publication No. US20040123343A1
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/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 116010
/ LENGTH: 528
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_19552C.1.pep
US-10-437-963-116010
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Query Match      85.4%; Score 35; DB 16; Length 528;
Best Local Similarity 87.5%; Pred.No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 MLAPTIPM 8
      |||||
Db      414 MLAPPIM 421
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RESULT 4

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US-10-101-662A-16
/ Sequence 16, Application US/10101662A
/ Publication No. US20030022198A1
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/ GENERAL INFORMATION:
/ APPLICANT: Kaelin Jr., William G
/ APPLICANT: Livingston, David A
/ APPLICANT: Kim, William
/ TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
/ TITLE OF INVENTION: Therapeutic Methods Thereof
/ FILE REFERENCE: 20363-009
/ CURRENT APPLICATION NUMBER: US/101,662A
/ CURRENT FILING DATE: 2002-03-19
/ PRIOR APPLICATION NUMBER: 60/277,425
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/277,431
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/277,440
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 60/332,493
/ PRIOR FILING DATE: 2001-11-09
/ PRIOR APPLICATION NUMBER: 60/345,131
```

; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-10-101-662A-16

Query Match 82.9%; Score 34; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
||| |||
Db 1 MLAPYIPM 8

RESULT 5
US-10-101-816-8
; Sequence 8, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Ivar, Mircea
; TITLE OF INVENTION: Mucins of Hypoxia Inducible Factor Alpha and Methods
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-10-287-670-16

Query Match 82.9%; Score 34; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
||| |||
Db 1 MLAPYIPM 8

RESULT 7
US-10-901-583-8
; Sequence 8, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29

; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-10-901-583-8

Query Match 82.9%; Score 34; DB 16; Length 19;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 6 MLAPYIPM 13

RESULT 8
US-10-287-670-25
; Sequence 25, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009C1P1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-25

Query Match 82.9%; Score 34; DB 14; Length 20;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 6 MLAPYIPM 13

RESULT 9
US-10-901-583-9
; Sequence 9, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-901-583-9

Query Match 82.9%; Score 34; DB 16; Length 34;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 13 MLAPYIPM 20

RESULT 10
US-09-922-958-5
; Sequence 5, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-5

Query Match 82.9%; Score 34; DB 9; Length 54;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 30 MLAPYIPM 37

RESULT 11
US-10-425-833-8
; Sequence 8, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-8

Query Match 82.9%; Score 34; DB 15; Length 409;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
||| |||
Db 240 MLAPYIPM 247

RESULT 12
US-10-425-833-9
; Sequence 9, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 466
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

Query Match 82.9%; Score 34; DB 15; Length 466;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
||| |||
Db 240 MLAPYIPM 247

RESULT 13
US-10-425-833-6
; Sequence 6, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael

; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-6

Query Match 82.9%; Score 34; DB 15; Length 538;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
||| |||
Db 369 MLAPYIPM 376

RESULT 14
US-10-264-049-2606
; Sequence 2606, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2606
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2606

Query Match 82.9%; Score 34; DB 15; Length 542;
Best Local Similarity 87.5%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLAPTIPM 8
||| |||
Db 277 MLAPYIPM 284

RESULT 15
US-10-425-833-7
; Sequence 7, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 7
; LENGTH: 595
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-7

Query Match      82.9%; Score 34; DB 15; Length 595;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      369 MLAPYIPM 376

RESULT 16
US-10-425-833-10
; Sequence 10, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 632
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-10

Query Match      82.9%; Score 34; DB 15; Length 632;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      240 MLAPYIPM 247

RESULT 17
US-10-205-342-13
; Sequence 13, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
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; OTHER INFORMATION: Protein: hypoxia-inducible factor-1 alpha
US-10-205-342-13

Query Match      82.9%; Score 34; DB 14; Length 823;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      561 MLAPYIPM 568

RESULT 18
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACTOR-1
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-922-958-4

Query Match      82.9%; Score 34; DB 9; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
Db      561 MLAPYIPM 568

RESULT 19
US-09-833-790-235
; Sequence 235, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-833-790-235

Query Match      82.9%; Score 34; DB 9; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPM 8
```

Db 561 MLAPYIPM 568
|||||

RESULT 20
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodges, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lijun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

Query Match 82.9%; Score 34; DB 9; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568
RESULT 21
US-09-902-941-330
; Sequence 330, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-330

Query Match 82.9%; Score 34; DB 9; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568
RESULT 22
US-09-849-626-330
; Sequence 330, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-330

Query Match 82.9%; Score 34; DB 9; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568
RESULT 23
US-09-967-388-4
; Sequence 4, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
; APPLICANT: JEFFEREY M. ARBEIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; FILE REFERENCE: UC077.001A
; CURRENT APPLICATION NUMBER: US/09/967,388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-4

Query Match 82.9%; Score 34; DB 10; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
|||||

Db 561 MLAPYIPM 568
RESULT 24
US-09-476-300-330
; Sequence 330, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-330

Query Match      82.9%; Score 34; DB 10; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPTM 8
Db      561 MLAPYIPM 568

RESULT 25
US-10-028-158-23
; Sequence 23, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-158-23

Query Match      82.9%; Score 34; DB 13; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPTM 8
Db      561 MLAPYIPM 568

RESULT 26
US-10-101-812-10
; Sequence 10, Application US/10101812
; Publication No. US20020192737A1
; GENERAL INFORMATION:
; APPLICANT: Ivan, Mircea
; APPLICANT: Kaelin Jr., William G
; TITLE OF INVENTION: Pharmaceuticals and Methods for Treating Hypoxia and
; TITLE OF INVENTION: Screening Methods Thereof
; FILE REFERENCE: 20363-014
; CURRENT APPLICATION NUMBER: US/10/101,812
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/277,425
```

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; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Target Peptide
US-10-101-812-10

Query Match      82.9%; Score 34; DB 13; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLAPTIPTM 8
Db      561 MLAPYIPM 568

RESULT 27
US-10-101-662A-9
; Sequence 9, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-101-662A-9

Query Match 82.9%; Score 34; DB 14; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPVIPM 568

RESULT 28

US-10-017-754-330
; Sequence 330, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-330

Query Match 82.9%; Score 34; DB 14; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPVIPM 568

RESULT 29

US-10-115-987B-14
; Sequence 14, Application US/10115987B
; Publication No. US20030148521A1
; GENERAL INFORMATION:
; APPLICANT: Bell, John C.; Stojdl, David F.;
; APPLICANT: Gray, Douglas A.; Sonnenberg,
; APPLICANT: Nahum, Lichty, Brian
; TITLE OF INVENTION: Conditionally Replicative and
; TITLE OF INVENTION: Conditionally Active Viruses
; FILE REFERENCE: 42630-0001
; CURRENT APPLICATION NUMBER: US/10/115,987B
; CURRENT FILING DATE: 2002-03-03
; PRIOR APPLICATION NUMBER: US60/281,781
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: EditPad
; SEQ ID NO 14
; LENGTH: 826
; TYPE: PRT
; ORGANISM: homo Sapiens
; PUBLICATION INFORMATION:
; AUTHORS: wang et al.

; JOURNAL: Proceedings of the National Academy of Sciences
; VOLUME: 92
; PAGES: 5510-5514
; DATE: 1995
US-10-115-987B-14

Query Match 82.9%; Score 34; DB 14; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPVIPM 568

RESULT 30

US-10-287-670-9
; Sequence 9, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009CIP1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-9

Query Match 82.9%; Score 34; DB 14; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPVIPM 568

RESULT 31

US-10-113-872-330
; Sequence 330, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.

; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-330

Query Match 82.9%; Score 34; DB 14; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPYIPM 568

RESULT 32

US-10-423-419-2
; Sequence 2, Application US/10423419
; Publication No. US20030176349A1
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/10/423,419
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US/09/383,581
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-419-2

Query Match 82.9%; Score 34; DB 14; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPYIPM 568

RESULT 33

US-10-283-017-330
; Sequence 330, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-017-330

Query Match 82.9%; Score 34; DB 15; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPYIPM 568

RESULT 34

US-10-901-583-18
; Sequence 18, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-583-18

Query Match 82.9%; Score 34; DB 16; Length 826;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAPTIPM 8
||| |||
Db 561 MLAPYIPM 568

RESULT 35

US-09-919-039-149
; Sequence 149, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113